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Pseudomonas

AAO26991 AAO26990 AAO26989 AAO26988 AAO26987 AAO26986

Pseudomonas aerug Histdine protein

Candida albicans Histdine protein Histdine protein

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                                                            August 14, 2003, 16:46:47 ; Search time 83 Seconds (without alignments) 260.082 Million cell updates/sec
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678
1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136
          5.1.6
Compugen Ltd.
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                            1107863 seqs, 158726573 residues
           GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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# ALIGNMENTS

osi histidine kina N. crassa osip pro osi+p amino acid s osi histidine kina Yeast Sini receive Herbicidally activ Putative P. abyssi Novel human diagno

Candida albicans S cos-1 histidine ki Candida albicans C

Human kinase-like

Herbicidally activ Eucalyptus grandis Histidine kinase C

AAB25534 AAW86007 AAY28484 AAW68522 AAY28481 AAY28483

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Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Scoring table:

Searched:

Title: Perfect score:

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AAB73275 ABB93422 ABP73292

AAB7

A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants protein; dehiscence; male sterile plant; DZ2 gene; oilseed rape; response regulator protein. Brassica response regulator protein D22. AA. ΰ AAY42637 standard; Protein; 136 Whitelaw 98GB-0006113. 99WO-GB00905 10-JAN-2000 (first entry) (BIOG-) BIOGEMMA UK LTD Wyatt P, Roberts JA, WPI; 1999-580449/49. N-PSDB; AAZ22974. Signal transduction shatter resistance; Brassica napus WO9949046-A1. 22-MAR-1999; 20-MAR-1998; 30-SEP-1999. AAY42637; RESULT 1 

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score	great	ter than or equal to the score of the	result being printed

and is derived by analysis of the total score distribution.

		Description	Brassica response	Brassica response	Arabidopsis thalia	Arabidopsis thalia	A. thaliana DZ2AT3	Brassica response	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia
SUMMAKIES		ID	AAY42637	AAY42653	AAG10549	AAG44439	AAY42645	AAY42652	AAG10550	AAG44440	AAG21089
			20	20	21	21	20	20	21	21	21
		Query Match Length DB	136	136	142	142	142	116	104	104	70
	dР	Query Match	100.0	100.0	79.4	79.4	76.0	9.69	64.5	64.5	44.4
		Score	678	678	538	538	515	472	437	437	301
		Result No.		2	m	4	ហ	9	7	60	ď

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B. napus DZ2 putative peptide sequence
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990S-0128714.
990S-0129845.
990S-0130077.
990S-0130449.
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990S-0134256.
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99US-0134941.
99US-0135124.
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99US-0126785.
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                                                                                                      Best Local Similarity 100.
Matches 136; Conservative
      the
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      sequence represents
                                               136 AA
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23-APR-1999;
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20-MAY-1999;
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08-APR-1999;
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                                                 Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1
                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents a B. napus response regulator protein DZ2.
                                                                                                                                                                                                                                                                                                                                                                       1 MATKSMGDIEKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                              A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal transduction protein; dehiscence, male sterile plant; D22 gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica response regulator protein DZ2 putative peptide sequence
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                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 678; DB 20; Length 136; Best Local Similarity 100.0%; Pred. No. 1e-67; Matches 136; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY42653 standard; Protein; 136 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 6; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 1; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-GB00905,
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N-PSDB; AAZ22977.
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61 SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKP 120
                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                  1 MATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGS
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Length 136;
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100.0%; Score 678; DB 20;
100.0%; Pred. No. 1e-67;
iive 0; Mismatches 0;
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PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 04-AUG-1999; 99US-0147204.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147202.

PR 05-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147493.

PR 10-AUG-1999; 99US-0147493.

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PR 12-AUG-1999; 99US-0147493.

PR 12-AUG-1999; 99US-0147493.

PR 12-AUG-1999; 99US-0149175.

PR 12-AUG-1999; 99US-0149175.

PR 23-AUG-1999; 99US-0149912.

PR 23-AUG-1999; 99US-014992.

PR 23-AUG-1999; 99US-011066.

PR 23-AUG-1999; 99US-011066.

PR 23-AUG-1999; 99US-011066.

PR 23-AUG-1999; 99US-011066.

PR 23-AUG-1999; 99US-015723.

PR 23-AUG-1999; 99US-015765.

PR 24-SEP-1999; 99US-015765.

PR 23-SEP-1999; 99US-015723.

PR 23-SEP-1999; 99US-015723.

PR 23-SEP-1999; 99US-015723.

PR 23-SEP-1999; 99US-015723.

PR 24-SEP-1999; 99US-015723.

PR 25-CCT-1999; 99US-015773.

PR 25-CCT-1999; 99US-01590.

PR 25-CCT-1999; 99US-01590.

PR 25-CCT-1999; 99US-01590.

PR 25-CCT-1999; 99US-01500.

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PR 25-CCT-1999; 99US-01500.

PR 25-CCT-1999; 99US-01500

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                                                                                                                                                                                                                                                                                          HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
                                                                                                                                                                                  1 MATKSMGDIEK-----IKKKL-NVLIVDDPLNLIHEKIIKAIGGISOTANNGEEAVII 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                             Gaps
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                                                                                                   79.4%; Score 538; DB 21; Length 142; 78.9%; Pred. No. 4.7e-52; ive 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 55668.
                                                                                                                                                                                                                                                                                                                                               115 HCLAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                                                   AAG44439 standard; Protein; 142 AA
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9905-0123180
9905-0123180
9905-0125788
9905-0125785
9905-0126785
9905-0126785
9905-0128134
9905-0130047
9905-0130047
9905-0131449
9905-0132485
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9905-0132485
9905-0132485
9905-0132485
9905-0132485
9905-0132485
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9905-0132485
9905-0132485
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000 (first entry)
                                                                                                   Query Match
Best Local Similarity 78.9
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2.
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08-APR-1999;
10-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
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30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                  25
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PR 02-Aug. 1999; 9908-0146586.

PR 02-Aug. 1999; 9908-0146588.

PR 04-Aug. 1999; 9908-0147302.

PR 05-Aug. 1999; 9908-0147302.

PR 05-Aug. 1999; 9908-0147302.

PR 05-Aug. 1999; 9908-0147302.

PR 10-Aug. 1999; 9908-0147302.

PR 11-Aug. 1999; 9908-014731.

PR 11-Aug. 1999; 9908-014731.

PR 11-Aug. 1999; 9908-0148319.

PR 20-Aug. 1999; 9908-0148319.

PR 20-Aug. 1999; 9908-0148366.

PR 20-Aug. 1999; 9908-014936.

PR 20-Aug. 1999; 9908-015246.

PR 20-Aug. 1999; 9908-015329.

PR 20-CCT 1999; 9908-015939; 9908-015939.

PR 20-CCT 1999; 99
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents a D22 A. thaliana homologue D22AT3 putative peptide sequence.
                                                                                                                                                                                  HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
                                                                                                                                                                                                  9
                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                               1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII
                                                                                                       Gaps
                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal transduction protein; dehiscence; male sterile plant; shatter resistance; oilseed rape; DZ2AT3 gene.
                                                                            79.4%; Score 538; DB 21; Length 142; 78.9%; Pred. No. 4.7e-52;
                                                                                                       Indels
                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                   A. thaliana DZ2AT3 putative peptide sequence.
                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...J Location/Qualifiers Misc-difference 57
                                                                                                                                                                                                                                                         121 HCLEKPLTKAKIFPLISHLFDA 142
                                                                                                                                                                                                                                          HCLAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                   AAY42645 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whitelaw C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unknown"
990S-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0006113.
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                Query Match 79.45
Best Local Similarity 78.99
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOG-) BIOGEMMA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wyatt P, Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-580449/49.
N-PSDB; AAZ22978.
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 26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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25-MAY-1
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                                                                                                                                                         55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
                                                                                                                                                                          1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal transduction protein; dehiscence; male sterile plant; D22B gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.6%; Score 472; DB 20; Length 116; 18.5; 18.80.2%; Pred. No. 8.4e-45; Live 11; Mismatches 12; Indels 0; Gaps
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Brassica response regulator protein DZ2B putative peptide sequence.
                                                                        .
6
                                       / Match 76.0%; Score 515; DB 20; Length 142; Local Similarity 76.1%; Pred. No. 1.7e-49; les 108; Conservative 8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
2
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                                                                                                                                                                                                                                            121 HCLEKPLTKAKIFPLISHLFDA 142
                                                                                                                                                                                                                                                                                                                   AAY42652 standard; Protein; 116 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-GB00905.
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                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-580449/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 AA;
               142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ22976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
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               Sednence
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                                          Query Match
                                                                     Matches
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Conservative

Local Similarity es 93; Conserv

Matches

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80
         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 21 VDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGVSTT
                                       81 KKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNRCLAKPLTKDKIIPLINQLMDA 136
                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 8917
                                                                                      AAG10550 standard; Protein; 104 AA
                                                                                                                                                                                                                                                          99US-0123180.
99US-0123548.
99US-0125788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0137724.
99US-0138094.
99US-0138540.
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99US-0132486.
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99US-0134219
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                                                                                                                     (first entry)
                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                    EP1033405-A2.
                                                                                                                     17-0CT-2000
                                                                                                                                                                                                                                                                                         29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                         16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                 23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                    06-SEP-2000.
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                                                                                                                                                                                                                                                    25-FEB-1999
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185-0139847 185-0139119 185-0139455 185-0139455 185-0139455 185-0139456 185-0139456 185-0139456 185-0139462 185-0139462 185-0139462 185-0139462	135-0139765 135-0139765 135-0140389 135-0140389 135-0140389 135-0140389 135-0140389 135-0140389 135-0140389 135-01429 135-014218	990x-0144632. 990x-0144814. 990x-0145086. 990x-0145087. 990x-0145087. 990x-0145087. 990x-0145192. 990x-0145192. 990x-0145192. 990x-0145181. 990x-0145218. 990x-0145218. 990x-0145218. 990x-0145913. 990x-0145913. 990x-0146386. 990x-0146386. 990x-0146386. 990x-0146386. 990x-0146386. 990x-0146386. 990x-0146386. 990x-0146386. 990x-0146386. 990x-0147302. 990x-0147302.
10N 1999	00000000000000000000000000000000000000	20 JUL 1999; 21 JUL 1999; 21 JUL 1999; 22 JUL 1999; 22 JUL 1999; 22 JUL 1999; 23 JUL 1999; 23 JUL 1999; 23 JUL 1999; 23 JUL 1999; 24 JUL 1999; 27 JUL 1999; 28 JU
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	Gaps
	Length 104; Indels 0;
	Score 437; DB 21; Pred. No. 5.9e-41; 6; Mismatches 10;
114408067787878	64.5%; arity 84.5%; onservative
10-AUG-1999; 11-AUG-1999; 13-AUG-1999; 13-AUG-1999; 14-AUG-1999; 15-AUG-1999; 16-AUG-1999; 17-AUG-1999; 18-AUG-1999; 20-AUG-1999; 21-AUG-1999; 21-AUG-1999; 22-AUG-1999; 23-AUG-1999; 24-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 28-P-1999; 29-SEP-1999; 29-SEP-1999; 20-CT-1999; 21-CT-1999; 21-CT-1999; 22-CT-1999; 23-CT-1999; 24-CT-1999; 25-CT-1999; 26-CT-1999; 27-CT-1999; 28-CCT-1999; 28-CCT-1999; 29-SEP-1999; 29-SEP-1999; 20-CT-1999; 20-CT-1999; 21-CT-1999; 22-CCT-1999; 23-CCT-1999; 24-CT-1999; 25-CCT-1999; 26-CCT-1999; 26-CCT-1999; 27-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999;	Query Match Best Local Similarit Matches 87; Conse
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34 IKAIGGISOTANNGEBAVIHRDGGSSFDLILMDKEMPRDQVSTTKKLREMEVKSMIV 93

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9905.0139455.9905.0139455.9905.0139455.9905.0139457.9905.0139457.9905.0139460.9905.0139461.9905.0139463.9905.0139395.9905.0139399905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9905.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.0140354.9005.01
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990S-0142055.
990S-0142390.
990S-0142803.
990S-0142920.
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990S - 0143624
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990S - 0144325
990S - 0144331
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990S - 0144333
990S - 0144834
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990S - 0145086
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990S-0145148
990S-0145218
990S-0145276
990S-0145918
990S-0145919
990S-01459519
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990S-0146389.
990S-0147038.
990S-0147204.
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99US-0148319.
99US-0148341.
     99US-0139453
99US-0139492
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99US-0147493
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 16 - JUN - 1999)

18 - JUN - 1999)
                                                                                                                                                                                                                                                  21 - 70N - 1999;
22 - 70N - 1999;
23 - 70N - 1999;
24 - 70N - 1999;
26 - 70N - 1999;
30 - 70N - 1999;
30 - 70N - 1999;
01 - 70L - 1999;
01 - 70L - 1999;
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05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
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11-AUG-1999;
12-AUG-1999;
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2 IIKTIGGISQTAKNGEEAVILHRDGEASFDLILMDKEMPERDGVSTTKKLREMKVTSMIV 61
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                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 55669.
                                                                                                                                                             AAG44440 standard; Protein; 104 AA.
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                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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30-APR-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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18-MAY-1999;
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16-JUN-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
           Arabidopsis thaliana protein fragment SEQ ID NO: 23518.
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19-APR-1999;
21-APR-1999;
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                                                                                                                                               RESULT 9
                                                                                                                                                                                     AAG21089
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   13-AUG-1999;
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9US-0139455	99US-0139456.	90S-0139457	903-0139438	90S-0139460	9US-0139461	9US-0139462	9US-0139463	905-0139/50 6116-0139763	903-0139/03	9115-0139899	903 0133633	905 0140353	2020 TO - SILO	0110-014083	5780 \$10 - 516	30S-0140991	9US-0141287	9US-0141842	9US-0142154	9US-0142055	9US-0142390	9US-0142803	9US-0142920	9US-0142977	9US-0143542	9US-0143624	9118-0144005	9US-0144085	9US-0144086	9115-0144325	9US-0144331	911S-0144332	9118-0144333	ASEA 10-210	0115-01144354	0118-0144030	000 01440000	7505570-506	9US-0144884	400-0144814 010-0148814	902 - 014 2086	9US-0145088	90S-0145085	90S-014508/	902-0145089	90S-0145192	9US-0145145	905-0143210	9TIS-0145276	9US-0145913	9US-0145918	9US-0145919	9US-0145951	9US-0146386	9US-0146388	9US-0146389	90S-0147038	908-014/204	908-0147302	908-014/192	047/#10-806	908-014/503	0147410 006	0116-0147935	1210 - 014 / 330	9118-0178319	0115-0140047	903-0148341	COCO # TO SOE	9115-0149368		
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PR 20.7405 | 9995 014427 |
PR 20.7407 | 9995 |
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                                                                    17-OCT-2000 (first entry)
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                          17-OCT-2000 (first entry)
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18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                               30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
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14 - MAY - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
18 - MAY - 1999;
                                                                                                                                  08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
                                                                                                                                                                             23-APR-1999;
23-APR-1999;
28-APR-1999;
06-SEP-2000.
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71 MPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLI 130 

a δŏ g RESULT 11 AAG21088

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990x5-0139461.
990x5-0139462.
990x5-0139463.
990x5-0139753.
990x5-013973.
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990x5-014918.
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10-AUG-1999;
11-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
16-AUG-1999;
17-AUG-1999;
                                                                                         02-70L-1999;
06-70L-1999;
09-70L-1999;
13-70L-1999;
14-70L-1999;
16-70L-1999;
16-70L-1999;
16-70L-1999;
16-70L-1999;
19-70L-1999;
19-70L-1999;
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23-JUL-1999;
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23-AUG-1999
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1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVII
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9905-0149930.
9905-0150864.
9905-0151065.
9905-0151066.
9905-0151080.
9905-0151080.
9905-0151080.
9905-0151930.
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9905-0151930.
9905-0154039.
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99US-0162142
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47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 HRDG 58
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| HRDG 64
 23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
01-SEP-1999;
115-SEP-1999;
115-SEP-1999;
115-SEP-1999;
16-SEP-1999;
22-SEP-1999;
22-SEP-1999;
23-SEP-1999;
23-SEP-1999;
                                                                                                                                                                                                                                                                                                              24 - SEP - 1999)

28 - SEP - 1999)

29 - SEP - 1999)

04 - OCT - 1999)

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28-OCT-1999;
29-OCT-1999;
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Best Local S:
Matches 47,
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54 9

RESULT 12 AAB25159 ID AAB25159 standard; Protein; 261 AA. XX AC AAB25159;

Gaps

(first entry)

27-NOV-2000

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ANA 9263 to AAA 9736 and AAB 25100 to AAB 25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Pinus radiate also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and contribent metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance and prolong the life of cut flowers or enhance of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life forest tree species giving long stretches of valuable knot-free clear coord which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals -
                                                                          Bucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.8%; Score 202; DB 21; Length 261; 36.5%; Pred. No. 3.7e-14; tive 34; Mismatches 37; Indels 2
                                              Pinus radiata cell signalling involved protein SEQ ID NO:127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 104-105; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENESIS RES & DEV CORP LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY42644 standard; Protein; 67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                                             99US-0162866
                                                                                                                                                                                                                                                                                      11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                           99us-0228986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-476052/41.
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nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AA;
                                                                                                                                                                                                                WO200042171-A1
                                                                                                                                                                               Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an arither in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents the partial fragment of B. napus DZ2B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RscC; antagonist; agonist; cytokinin receptor; receptor; signal transduction; histidine kinase; hormone; cell division; cell differentiation; agriculture; growth regulator; harvest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAT--KSMGDIEK----IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                  Signal transduction protein; dehiscence; male sterile plant; DZ2B gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 28.4%; Score 192.5; DB 20; Length 1 Similarity 65.7%; Pred. No. 6.7e-14; 44; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli RscC receiver region of histidine kinase.
         Brassica napus DZ2B partial fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG70785 standard; Protein; 118 AA
                                                                                                                                                                                                                                                       Wyatt P, Roberts JA, Whitelaw C;
                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 5; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-2002; 2002EP-0005749
                                                                                                                                                                    99WO-GB00905
                                                                                                                                                                                                98GB-0006113
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                                                                                                                                                                                                                           (BIOG-) BIOGEMMA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 IHRDGGS 60
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                                                                                                                                                                                                                                                                                     WPI; 1999-580449/49.
N-PSDB; AAZ22975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                   Brassica napus.
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                                                                                                                                                                                                   20-MAR-1998;
                                                                                                             W09949046-A1
                                                                                                                                         30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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05-JUL-2002; 2002WO-US23242

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The invention discloses a method for analysing antagonist or agonist

activity to a cytckinin receptor. The method comprises bringing a
candidate substance into contact with a transformed cell, in which a DNA
candidate substance into contact with a transformed cell, in which a DNA
candidate substance into contact with a transformed cell, in which a DNA
concoling the receptor has been introduced, and then measuring the
existence, or the quantity, of the intracellular signal transduction from
the receptor expressed in the cell. The cytchinin receptor comprises an
extracellular region of the receptor, transmembrane regions, a histidine
kinase region and a receiver region of the kinase. The transmembrane
cell division and differentiation of higher plants. The method is used
to cell division and differentiation of higher plants. The method is used
for analysing agonist or antagonist activity to a cytckine receptor. A
substance with agonist or antagonist activity to a cytckine receptor. A
substance with agonist or antagonist activity to a cytckine receptor on be
used, in agriculture, as a plant growth regulator, e.g. after harvest.
The advantage is that the candidate substances do not need to be prepared
in such large amounts as in previous methods and that the method avoids
the immensely long time to observe and evaluate the growth of the plant
and the physicalogical changes of the plant after spraying. The sequence
presented is the B. coli receiver region of histidine kinase which can
transmit signals to the cytokinin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; PvrR; variant Pseudomonas; microorganism; gram negative; phenotype-mediated antibiotic-resistance; gram-positive; bacterial infection.
                                                                                                                                                                                                                             Analyzing agonist or antagonist activity of a substance for use as a plant growth regulator, comprises measuring intracellular signal transduction from a cytokinin receptor expressed in a cell contacted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
25.3%, Score 171.5; DB 23; Length
Best Local Similarity 33.9%; Pred. No. 3.2e-11;
Matches 37; Conservative 32; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa PvrR related protein, SEQ ID No 4.
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                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 42; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO26983 standard; Protein; 471
                                                                                                  (SUMO ) SUMITOMO CHEM CO LID.
           15-MAR-2001; 2001JP-0073812.
29-JUN-2001; 2001JP-0198639.
29-JUN-2001; 2001JP-0198640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                   with the test substance
                                                                                                                                                                                         WPI; 2002-693041/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003004691-A2
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                                                                                                                                               Kakimoto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              φ
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Gaps

3;

16-JAN-2003

DB 23; Length 118;

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16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated polypeptide comprising a PvrR (variant Pseudomonas) amino acid sequence having at least 50 % identity to a 399 residue amino acid sequence, given in the specification, where expression of the polypeptide, in a microorganism, affects phenotypendiated antibiotic resistance in the microorganism. The methods and compositions of the present invention are useful for the diagnosis, prevention and treatment of gram negative or gram-positive bacterial infection. This sequence repersents a Pseudomonas protein used in the exemplification of the invention.
                                                                                                                                                                                                                     New isolated PvrR polypeptide and polynucleotide that regulates bacterial biofilm formation, useful for the diagnosis, prevention and treatment of gram-negative or gram-positive bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%; Score 156.5; DB 24; Length 471; 35.8%; Pred. No. 9.9e-09; Live 22; Mismatches 43; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .9e-09;
tes 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 14, 2003, 16:50:31
                                                                                                                                                                                                                                                                                                Disclosure, Fig 5E; 185pp; English.
                                              06-JUL-2001; 2001US-303286P.
16-APR-2002; 2002US-373233P.
                                                                                                   (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
                                                                                                                                      Drenkard E;
                                                                                                                                                                       WPI; 2003-221608/21.
N-PSDB; AAL55304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471 AA;
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                                                                                                                                        Ausubel FM,
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US-09-228-986-127
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Sequence 31338, A
Sequence 29359, A
Sequence 20355, A
Sequence 36, Appli
Sequence 17557, A
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 234, Appli
Sequence 2843, Appli
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27075, A
18, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                 Description
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                                                      August 14, 2003, 16:46:47; Search time 29 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-252-991A-31338
US-09-252-991A-20395
US-09-252-991A-20395
US-08-843-530B-36
US-08-843-530B-6
US-08-843-530B-6
US-08-843-530B-4
US-08-843-530B-4
US-08-843-530B-3
US-09-252-991A-28143
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US-09-252-911A-27075
US-08-843-530B-18
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US-09-107-532A-6769
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US-09-112-450-2
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Sequence 7973, Application US/09328352
Patent No. 6562958
CENERAL INFORMATION: BALLAING ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BALLAINI FOR DIAGNOSTICS AND THERAPRUTICS
TITLE OF INVENTION: BALLAINI FOR DIAGNOSTICS AND THERAPRUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7973
LENGTH: 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 127, Application US/09228986
Patent No. 6399198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieus
TITLE OF INVENTION: Compositions Isolated from Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 130
Sequence 6073, Appagequence 22212, A Sequence 21677, A Sequence 31677, A Sequence 23765, Appagemence 114, Appagemence 17904, A Sequence 6189, Appagemence 6189, Appagemence 6146, Appagemence 6146, Appagemence 6146, Appagemence 5137, Appagemence 5137, Appagemence 5040, Appagemence 2217, Appagemence 2217, Appagemence 2217, Appagemence 2214, Appagemence 2217, Appagemence 2214, Appagementer 2214, 
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EATRQLESMGVKTPIVALTA-NTLQSDKDLFFEAGVDDFQSKPLSRDRLVQLLDQ 249
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US-09-328-352-6073

US-09-252-91R-22232

US-09-252-91R-22232

US-09-252-91R-31677

US-09-252-991R-31677

US-09-252-991R-33765

US-09-252-991R-33765

US-09-252-991R-16981

US-09-252-991R-16981

US-09-107-532R-6859

US-09-138-352-7397

US-09-107-532R-6859

US-09-138-352-7397
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US-09-328-352-7973
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            TYPE: PRT ORGANISM: Pinus radiata
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US-09-328-352-7973
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us-09-646-679-15.rai

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COMPUTER READABLE FORM:
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LENGTH: 1627
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; SEQ ID NO 29359
; LENGTH: 947
                                                   TYPE: PRT
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APPLICANT: MATC J. RUDenfield et al.
APPLICANT: MATC J. RUDenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1988-02-18
PRIOR FILING DATE: 1988-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                               674 LHILAVDDHLPNLIVLEALLGELNVKTTKALSGQEALNIIQERIDQKLKPFDLVFMDIQM 733
                                                                                                                                                                                                                  72 PERDGVSTTKKLREM-----EVKSMIVGVT--SLADNEEERRAFMEAGLNHCLAKPLTK 123
                                                                                                                                                                                                                                                868 ARSGVAEVEERKEARALSILLAEDHPFNRLTLTMQLESLGHRVTSTEDGEEA--FERWQG 925
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                                                                                                                       16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSS----FDLILMDKEM 71
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                  Query Match 22.5%; Score 152.5; DB 4; Length 946; Best Local Similarity 30.2%; Pred. No. 3.4e-09; Matches 39; Conservative 34; Mismatches 41; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 22.1%; Score 150; DB 4; Length 1014;
Best Local Similarity 25.5%; Pred. No. 7.4e-09;
Matches 35; Conservative 36; Mismatches 56; Indels 10; Gaps
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; Sequence 31338, Application US/09252991A
; Patent No. 6551795
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US-09-252-991A-29359
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LENGTH: 1014
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                 14 KKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                 18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                          77 VSTTKKLREMEVKSMI--VGVTSLADN--BEERRAFMEAGLNHCLAKPLTKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                    74 RDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKD 124
                                                                                                                                43; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.7%; Score 147; DB 4; Length 1627; 31.9%; Pred. No. 3.3e-08; tive 26; Mismatches 45; Indels 8
                                                                        21.8%; Score 148; DB 4; Length 947; 28.8%; Pred. No. 1.1e-08; tive 33; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osmosensing Histidine Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/08843530B
Patent No. 593306
GENERAL INFORMATION
APPLICANY: Selitrennikoff, Claude
APPLICANY: Adnan, Jacqueline
APPLICANY: Adnan, Jacqueline
APPLICANY: Alax, Lisa A.
APPLICANY: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinas,
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 20395, Application US/09252991A ; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Pseudomonas aeruginosa US-09-252-991A-20395
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29359
                                                                                                     Local Similarity 28,8% (es 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 31.9%
nes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
COUNTRY: United State
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-252-991A-20395
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1075 ATPSLAD---NTKSFEILLAEDNTVNQRLAVKILEKYHHVVTVVGNGEEAVEAVKR---K 1128
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95 EATRLIRREERAQGWPRVPIVALTAHILD--EHRRAGIEAGMDAYLGKPVDRAELYATLE 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IEM PC compatible
COMPUTER: IEM PC COMPATIBLE
CORTURENT SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NO PATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
                                                                                                                                                                                                                                                       APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.6%; Score 139.5; DB 2; 31.1%; Pred. No. 1.8e-07; Live 28; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                         E: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 220 MOLLOS.
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Selitrennikoff, Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
                                                                                                                                                                                              Sequence 6, Application US/08843530B Patent No. 5939306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:11| :: :| |
|1188 YLSKPLQQNHLIQTI 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397 8338 INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%
Best Local Similarity 31.1%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                  132 QLM 134
                                                                                        153 RLL 155
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US-08-843-530B-6
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APPLICANT: MARCA IS RUBEnfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STIKKLREME-----VKSMIVGVIS-LADNEEERRAFMEAGLNHCLAKPLIKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 SSFDLILMDKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 DIEKIKKKLNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Indels
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.2%; Score 144; DB 4; 30.9%; Pred. No. 2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.4%; Score 145; DB 2; Best Local Similarity 29.0%; Pred. No. 3.8e-08; Matches 40; Conservative 40; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 28; Mismatches
                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MACKINGTH, KARRIN T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,397-838
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 mmino acids
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Sequence 17557, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                    омыжк: US/08/843,530B
16-APR-1997
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US-09-252-991A-17557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 KPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                            FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-843-530B-36
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116 CLAKPLTKDKIIPLI 130
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      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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FILING DATE: 16-APR
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not
      MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
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ADDRESSEE: Medien & Carroll, ilp
STREBT: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/ACENT INPORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                       California
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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1188 YLSKPLQQNHLIQTI 1202
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MOLECULE TYPE: peptide
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US-08-843-530B-4
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                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
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1075 ATPSLAD---NTKSFEILLAEDNIVNQRLAVKILEKYHHVVTVVGNGEEAVEAVKR---K 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Indels 13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Selitrennikoff, Claude
APPLICANT: Alan, Jacqueline
APPLICANT: Alan, Lisa A.
APPLICANT: Alan, Malvin I.
TITLE OF INVENTION: OSEOGENSING Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STREET: 220 M
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MACKIDITC LAGRARIA TON
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMONICATION INFORMATION:
TELEPHONE: (415) 705-8410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/843,530B
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC COMPATION
COMPUTER: PC-DOS/MS-DOS
COMPANYING SYSTEM: PC-DOS/MS-DOS
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RESULT 15
US-09-252-991A-26112
; Sequence 26112, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT;
CRGANISM: Lactobacillus rhamnosus
US-09-634-238-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25928
Christensson, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TKDKI 126
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
TILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLICING DATE: 1999-02-18
PRIOR PLICING DATE: 1998-02-18
PRIOR PLICING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
LENGTH: 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : :|:|: || : ||: || | : 182 || : || : || : || : ||: || : ||: || : ||: || : ||: || : ||: || : ||: || : ||: ||: || : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFMEAGLNH 115
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20.6%; Score 139.5; DB 4; Length 1441;
Best Local Similarity 28.8%; Pred. No. 2.2e-07;
Matches 34; Conservative 30; Mismatches 43; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.6%; Score 139.5; DB 2; Length 1298; Best Local Similarity 31.1%; Pred. No. 1.8e-07; Matches 42; Conservative 28; Mismatches 52; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28143, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 220, Application US/09634238
Patent No. 654472
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Lubbers, Leonard, N.
APPLICANT: Lubbers, Mark W.
APPLICANT: Dekker, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
    TELEPHONE: (415) 705-8410
TELEFAX: (415) 39-8338
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGHH: 1298 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1188 YLSKPLQQNHLIQTI 1202
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US-09-252-991A-28143
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US-09-634-238-220
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RESULT 14
0.09-252-991A-25928

Sequence 25928, Application US/09252991A

Sequence 25928, Application US/09252991A

Sequence 25928, Application US/09252991A

Setent No. 6551795

Fatent No. 6551795

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ASROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ASROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

WUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25928

LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 DVTCKIREEKIQTPIMILTA-KDNETDKIVGLELGADDYVTKPFSPREIIARIKAI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
m
APPLICANT: Holland, Ross
APPLICANT: Holland, Ross
APPLICANT: Croole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, prince of Invention
TITLE OF INVENTION: PROPER SECURION NUMBER: US/09/634,238
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 220
LENGTH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.0%; Score 135.5; DB 4; Length 760; Best Local Similarity 28.0%; Pred. No. 2.5e-07; Matches 35; Conservative 31; Mismatches 54; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.4%; Score 138.5; DB 4; Best Local Similarity 30.2%; Pred. No. 2e-08; Matches 35; Conservative 31; Mismatches 47;
```

FALENC NO. 90.347103.

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: 02/09/252,991A
CURRENT APPLICATION NUMBER: 05 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26112
LENOTH: 860
TYPE: PRT
ORGANISM: PSEUdomonas aeruginosa

61 SFDLILMDKEMPERDGVSTTKKLREM----EVKSMIVGVTSLADNEEERRAFMEAGLNHC 116

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1 MATKSMGDIEKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60

Query Match

20.0%; Score 135.5; DB 4; Length 860;
Best Local Similarity 26.5%; Pred. No. 3e-07;
Matches 36; Conservative 35; Mismatches 56; Indels 9

US-09-252-991A-26112

Gaps 6

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Search completed: August 14, 2003, 16:51:53 Job time : 30 secs
                                                                 ||||| :|: ::::
LAKPFHRDELKAILDR 852
                                             117 LAKPLTKDKIIPLINQ 132
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August 14, 2003, 16:49:07 ; Search time 55 Seconds (without alignments) 323.935 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-646-679-15 678 1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136 Title: Perfect score: Sequence:

Scoring table:

492763 seqs, 131003257 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\* Database :

cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

cgn2\_6/ptodata/1/pubpaa/PCUI2\_PUBCOMB.pep:\*

cgn2\_6/ptodata/1/pubpaa/PCUI2\_PUBCOMB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US098\_PUBCOMB.pep:\*

cgn2\_6/ptodata/1/pubpaa/US098\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.ppp:\*
/cgn2\_6/ptodata/1/pubpaa/US10A\_UBDCOMB.ppp:\*
/cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.ppp:\*
/cgn2\_6/ptodata/1/pubpaa/US10\_LEW\_PUB.ppp:\*
/cgn2\_6/ptodata/1/pubpaa/US10\_LEW\_PUB.ppp:\*
/cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.ppp:\*
/cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.ppp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Sequence 127, App	Sequence 8, Appli	Sequence 328, App	Sequence 909, App	Sequence 332, App	Seguence 366, App	Sequence 2, Appli	Seguence 7, Appli	Sequence 10049, A	Seguence 4, Appli	Sequence 17, Appl	Sequence 11131, A	Sequence 12532, A	Sequence 9975, Ap	Sequence 13783, A
	QI	US-10-101-464A-127	US-09-918-508-8	US-09-801-368-328	US-10-101-464A-909	US-09-801-368-332	US-09-801-368-366	US-10-126-120-2	US-09-918-508-7	US-10-156-761-10049	US-09-424-951-4	US-10-135-322-17	US-09-815-242-11131	US-10-156-761-12532	US-10-156-761-9975	US-09-815-242-13783
	93	15	10	10	15	10	10	15	10	15	10	14	σ	15	15	თ
	Query Match Length DB ID	261	118	622	1018	1220	712	974	125	1829	1081	2150	227	203	227	232
æ	Query Match 1	29.8	25.3	22.1	21.5	21.4	21.2	20.3	20.2	19.5	18.9	18.8	18.7	18.6	18.5	18.4
	Score	202	171.5	150	146	145	143.5	137.5	137	132	128	127.5	126.5	126	125.5	124.5
	Result No.		7	8	4	Ŋ	Ø	7	ω	σ	10	11	12	13	14	15

Sequence 2, Appli	Sequence 4, Appli	Sequence 54, Appl	Sequence 8624, Ap	Sequence 12602, A	Seguence 956, App	Sequence 12098, A	Seguence 13746, A	Seguence 11629, A	Sequence 10420, A	Sequence 958, App	Sednence 979, App	Sequence 19, Appl	Sequence 2, Appli	Sequence 13096, A	Sequence 114, App	Sequence 11581, A	equence 27, App	0048	637(	equence 24,	equence 4, 1	ednence 30'	eguence 10,	equence 117,	equence 827,	976	29	18	
-11	US-10-116-048	0S-09-769-78	US-10-156-761-8624	156-76	101-46	15-242	126-76	15-242	15-242	US-10-101-46	101-46	135-32	918	156-761-130	101	156-761-115	US-10-100-294A-2	US-10-156	US-09-738-626-637	US-09-819	US-09-918	US-10-135	OS-09-819	US-10-101-464A-11	US-10-101	US-10-101-464A-97	US-10-135-322-2	US-10-135-322-18	GS
14	14	11	15	15	15	σ	15	σ	6	15	15	14	10	15	15	15	12	15	10	11	10	14	11	15	1.5	15	14	14	15
971	2471	18	1447	248	1044	24	218	222	232	890	27	1173	17	38	762	243	747	228	235	699	1036	104	573	599	816	1240	100	1092	197
			18.1							17.4					-		16.7											16.2	
124	124	123.5	123	122.5	122.5	122	121.5	120.5	118.5	118	118	117.5	117.5	117	115	114.5	113	112	111.5	111	111	110.5	110	110	110	110	109.5	109.5	107
16	17	18	19	20	21	22	23	24	25	5.6	27	28	29	30	31	32	33	34	E C	36	37	38	6°E	40	41	42	43	44	45

# ALIGNMENTS

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Length 622;
                22.1%; Score 150; DB 10;
28.1%; Pred. No. 7.3e-08;
tive 32; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 DLILMDKEMPERDGVSTTKKL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-801-368-332
Sequence 332, Application US/09801368
Fatent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 ----- 1PLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 ILIRYLKDRIPLCEQ 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Eucalyptus grandis
US-10-101-464A-909
                             Query Match 22.1%
Best Local Similarity 28.1%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.5%
Best Local Similarity 25.2%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-101-464A-909
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Patent No. US2002017716241

GENERAL INVORMATION:
APPLICANT: KAKIMOTO, TATSUO
APPLICANT: HIGHORY, MASATUKI
APPLICANT: INOUE, TSUTONU
TITLE OF INVENTION: TO CTTOKININ RECEPTOR
FILE REFERENCE: Q65478
CURRENT APPLICATION NUMBER: US/09/918,508
CURRENT APPLICATION NUMBER: US/09/918,508
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: JP 2001-073812
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLIIMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.3%; Score 171.5; DB 10; Length Best Local Similarity 33.9%; Pred. No. 3.2e-11; Matches 37; Conservative 32; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 328, Application US/09801368 Patent No. US20020128250A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQ ID NO 328

: LENGTH: 622

: TYPE: PR

; ORGANISM: Saccharomyces cerevisiae

US-09-801-368-328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Escherichia coli
US-09-918-508-8
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-801-368-328
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US-09-918-508-8
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Sequence 909, Application US/10101464A

publication No. US20030046728A1

GENERAL INFORMATION:
APPLICANT: Rieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPRENCE: 11000.10262
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT PILING DATE: 2002-03-18
PRIOR PILING DATE: 1999-01-10.
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989

SOFTHARE: FastSEQ for Windows Version 4.0

LENGTH: 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  858 SSSIVEEPKPKPKPKILLIVEDNKINVMVTQSMMKQLGHSMDVVNNGVEAV--HAVQQSTY 915
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                                                                                                                                                              68
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                                       12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Gaps
  Gaps
Indels 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.5%; Score 146; DB 15; Length 10
25.2%; Pred. No. 4e-07;
ive 35; Mismatches 53; Indels
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FESULO.2
Sequence 2, Application US/10126120
Sequence 2, Application WS/10126120
Sequence 2, Application No. US2030108526A1
Sequence 2, Application No. US2030108526A1
SENERAL INVORMATION:
APPLICANT: Takel, Kentan
APPLICANT: Takel, Kentan
APPLICANT: Davis, MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FAC
FILE REFERENCE: 11127-004001
CURRENT PAPLICATION NUMBER: US/10/126,120
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 885 EMDGFEATGQIRQMELKANEERKNKLASIEGSTTAEYHLPVLAMTADVIQATYEECIKSG 944
                                                                                                                                                                                                 ...-----MIVGVTSLADN 101
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Patent No. US20020177162A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RIGHT, MASAVIKI
APPLICANT: INOUE, TSUTOMU
APPLICANT: INOUE, TSUTOMU
APPLICANT: TOUE, TSUTOMU
APPLICANT: TOUE, TSUTOMU
APPLICANT: OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY
TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY
FILE OF INVENTION: TO CYTOKININ RECEPTOR
FILE REFERENCE: Q65478
CURRENT APPLICATION NUMBER: US/09/918,508
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                10 EKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDK
                                                                                                                     42; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.3%; Score 137.5; DB 15; Length 974; 24.6%; Pred. No. 3.2e-06; Live 32; Mismatches 46; Indels 29;
                                                                    DB 10; Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 ERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRA----
                                                                      Query Match 21.2%; Score 143.5; DB 1
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                945 MDGYVSKPFDEEQLYQAVSRLV 966
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                                                                                                                                                                                                                                                                           70 EMPERDGVSTIKKLREMEVKS----
                                                                                                                                                                                                                                                                                                                                                                          102 EEERRAFMEAGLNHCLAKPL 121
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.68
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Zea mays US-10-126-120-2
                     US-09-801-368-366
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US-09-918-508-7
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                                                   APPLICANT: No. USEC.__
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Sunamers, Eric
TILE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REPERICE: 109272.147
CURRENT PELLING DATE: 2001-03-07
FILE REPERICE: 2001-03-07
FILE CONTROL OF SECONDATE: 1099-10-20
FRIOR FILING DATE: 1999-10-20
FRIOR FILING DATE: 1999-10-20
FRIOR FILING DATE: 1999-10-20
SOFTWARR: Patentin Version 3.0
SEQ ID NO 332
TENGTH: 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1136 ENYNMIFWDVQMPKVDGLLSTKMIRRDLGYTSPIVALTAFADDSNIKEC-LESGMNGFLS 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1080 DDDKNETSVKILVVEDNHVN----QEVIKRMLNLEGIENIELACDGQEAFDKVKELTSKG 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 SSFDLILMDKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 DIEKIKKKLNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.4%; Score 145; DB 10; Length 1220; Best Local Similarity 29.0%; Pred. No. 6.6e-07; Matches 40; Conservative 40; Mismatches 44; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
SEQ ID NOS: 440
SEQ ID NOS: 440
SEQ ID NO 366
LENGTH: 712
TYPE: PRI
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Patent No. US20020128250A1
GENERAL INFORMATION
APPLICANT Busby, Robert
APPLICANT Hecht, Peter
APPLICANT Holtzman, Doug
APPLICANT Madden, Kevin
APPLICANT Madden, Kevin
APPLICANT Madden, Kevin
APPLICANT Mann, Thea
APPLICANT Mine, Tool
APPLICANT Shows John
APPLICANT Shows Solie
APPLICANT Solama, Solie
APPLICANT Slywa, Jeff
APPLICANT Sliva, Jeff
                             Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : : | : | 1195 KPIKRPKLKTILTEFCAA 1212
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  Madden, Kevin
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US-09-801-368-366
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LENGTH: 2150
TYPE: PRT
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US-10-135-322-17
                                                                                                                                                                                                                                                                                      LENGTH: 1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 DGVSTTKKLREME--VKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMDKEMPER 74
                                                                                                                                                                                                                                                                                                          DKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                   16 LNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGGSSFDLILM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                       Length 125;
                                                                                                                                                                                           37; Indels
                                                                                                                                                     20.2%; Score 137; DB 10;
29.4%; Pred. No. 2.1e-07;
tive 38; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION NO. US2003011901841
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENDE: 249-262
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-274089
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Streptomyces avermitilis US-10-156-761-10049
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US-09-424-951-4
; Sequence 4, Application US/09424951
; Parent No. US20020137034A1
                                                                            TYPE: PRT
CRGANISM: Saccharomyces cerevisiae
US-09-918-508-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.59
Best Local Similarity 31.59
Matches 39; Conservative
                                                                                                                                                         Query Match 20.2%
Best Local Similarity 29.4%
Matches 37; Conservative
NUMBER OF SEQ ID NOS: 22
                     SOFTWARE: Patentin Ver.
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US-10-156-761-10049
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                                        SEQ ID NO 7
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865 SQNSDESVRYK---ILLAEDNLVNOKLAVRILEKQGHLVEVVENGLEAYEAIKR---NKYD 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 KKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 SMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFD
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         APPLICANT: SOLL, DAVID R.

TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE, TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE, TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE, CURRENT APPLICATION NUMBER: US/09/424,951

CURRENT APPLICATION NUMBER: DC/098/11658

PRIOR PELLING DATE: 1998-06-06

PRIOR PILLING DATE: 1999-06-06

PRIOR FILLING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTIN VOI: 2.1

SEG ID NO 4

LEMANDE OF SEQ ID NOS: 7

SEG ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match Local Similarity 28.3%; Score 128; DB 10; Length 1081; Local Similarity 28.3%; Pred. No. 4e-05; les 43; Conservative 31; Mismatches 48; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 ERDGVSTTK----KLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APELICANT: MAHONEN, AP
APPLICANT: MAHONEN, AP
APPLICANT: RAUPPINEN, L
APPLICANT: RIKONEN, M
TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
FILE REPERENCE: 5914-086-999
CURRENT APPLICATION NUMBER: US/10/135,322
CURRENT PILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  976 KGMDDYVSKPLKPKLLMQTIKKCIHNINQLKE 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10135322
Publication No. US20020173017A1
GENERAL INFORMATION:
APPLICANT: BENERY, PN
APPLICANT: HELARIUTTA, Y
APPLICANT: SRIKANTHA, THYAGARAJAN APPLICANT: SOLL, DAVID R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-10-135-322-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
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Best Local Similarity 32.5
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Candida albicans US-09-424-951-4
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75 DGVSTTKKLREMEVKSMIVGVTSLAD-------NEEERRAFMEAGLNHCLA 118
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                                                                                                                                                                                                                                                                                                                                                                                           17 NVLIVDDDPLNLIHEKIIKAIGGISQ--TANNGEEAVIIHRDGGSSFDLILMDKEMPER 74
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                                                                                                                                                                                                                                                                           Length 203;
                                                                                                                                                                                                                                                                    Query Match
18.6%; Score 126; DB 15; Length 20
Best Local Similarity 29.5%; Pred: No. 6.5e-06;
Matches 36; Conservative 20; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.5%; Score 125.5; DB 1
29.2%; Pred. No. 8.6e-06;
tive 28; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CENEERAL INFOGRATION
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SENGTH: 227
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF, SEQ ID NOS: 15109
SEQ ID NO 12532
LENGTH: 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Streptomyces avermitilis US-10-156-761-9975
                                                                                                                                                          TYPE: PRT; ORGANISM: Streptomyces avermitilis US-10-156-761-12532
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Best Local Similarity 29.2%
Matches 38; Conservative
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US-10-156-761-9975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
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                                                                                                                                                                                                                                           APPLICANT: Chicach, ACCELL
APPLICANT: Chicach, ACCELL
APPLICANT: Cyskind Judith W.
APPLICANT: Zyskind Judith W.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H Howard
TITLE OF INVENTION: Dentification of Essential Genes in
TITLE OF INVENTION: Dentification of Essential Genes in
TITLE OF INVENTION: DENTIFY. 101.A
CURRENT FILING DATE: 2001-03-21
PRIOR PPLICATION NUMBER: 60/206, 848
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF EED ID NOS: 14110
SEC ID NO 1131
MANDER OF EED ID NOS: 14110
SEC ID NO 1131
MANDER OF END DATE: 201-02-16
MANDER OF ED ID NOS: 14110
SEC ID NOS: 14110
MANDER OF ED ID NOS: 14110
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18.7%; Score 126.5; DB 9;
Best Local Similarity 29.1%; Pred. No. 6.7e-06;
Matches 34; Conservative 30; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHTYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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Sequence 12532, Application US/10156761
Publication No. US/20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                Sequence 11131, Application US/09815242
Patent No. US20020061569A1
PATERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Haemophilus influenzae US-09-815-242-11131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
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65 ILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKD 124
                                                                                                                                                 4 EESRKPARVVVADD---QTVVREGIVMLIGILPGIEVVGAAGDGHEAVKLVAE--LNPDV 58
10 EKIKKKINVLIVDDDPLNLIIHEKIIKAIG---GIS--QTANNGEEAVIIHRDGGSSFDL
                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-815-242-13783
; Sequence 13783, Application US/09815242
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Query Match 18.4%; Score 124.5; DB 9; Length 232; Best Local Similarity 28.2%; Pred. No. 1.1e-05; Matches 33; Conservative 31; Mismatches 48; Indels 5;
                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Ammoto, Robert T.
APPLICANT: 2000-03-21
APPLICANT: APPLICATION NUMBER: 60/191,078
APPLICANT: 2000-05-23
APPLICANT: APPLICATION NUMBER: 60/203,727
APPLICANT: APPLICATION NUMBER: 60/203,727
APPLICANT: APPLICATION NUMBER: 60/203,727
APPLICANT: APPLICATION NUMBER: 60/203,938
APRIOR FILLING DATE: 2000-10-23
APPLICANT: APPLICATION NUMBER: 60/203,938
APRIOR FILLING DATE: 2000-10-23
APPLICANT: APPLICATION NUMBER: 60/204,308
APRIOR FILLING DATE: 2001-02-16
APPLICANT: APPLICATION NUMBER: 60/205,931
APPLICANT: APPLICATION NUMBER: 60/205,931
APPLICANT: APPLICATION NUMBER: 60/205,931
APRIOR FILLING DATE: 2001-02-16
APPLICANT: APPLICATION NUMBER: 60/205,931
APPLICANT: APPLICATION NUMB
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US-09-815-242-13783
Patent No. US20020061569A1
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78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLM 134 δy

g

5; Gaps

Search completed: August 14, 2003, 16:59:18 Job time : 56 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 14, 2003, 16:46:47; Search time 39 Seconds (without alignments) 335.357 Million cell updates/sec US-09-646-679-15 678 1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283308 segs, 96168682 residues Searched: 283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	histidine kinase h	rotein ev	sensor f	probable sensor fo	istidin		prote	sensor for ctr cap	hypothetical prote	¥	sensory box histid	aerobic respiratio	response regulator		C	sensory box histid	chemotaxis protein	sensory box histid	response regulator	sensor histidine k	sensory box histid	Ψ	axi	hist	transduct	sensory transducti	aerobic respiratio	two-component sens	cell wall assembly
SUMMARIES	T08875	G65010	A91035	C85879	H87640	AD0790	BVECCC	C91017	E85861	AD0149											A87617	54	25	56	10	S75525	060	AB0032	34
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probable sensor/re aerobic respiratio	aerobic respiratio aerobic respiratio	sensor/response re probable two-compo	SLN1 protein – yea sensor histidine k	sensor histidine k	SSK1 protein - yea	sensor histidine k sensory box histid	sensor protein [im	probable response	two-component regu
A83324 RGECAR	A91140 D85985	E83529 F83153	S48387 E87460	C82424	S64828	C87575 D87559	AI0860	H97516	B41863
7.7	01 01	0 0	03 03	010	4 (4	01 C1	~	C)	C3
992	778	925 1212	1220	857	712	693 637	918	152	929
22.1 22.1	22.1	21.8	21.4	21.2	21.2	21.1	21.0	20.9	20.9
150	149.5 149.5	148 147	145	44.	143.5	143	142.5	142	142
30 31	3.2	9. 9. 4. 73	36	. w c	4 4 9 0	412	43	44	4.5

# ALIGNMENTS

RESULT 2 G65010

Solutions protein evgS (EC 2.7.3.-) precursor - Escherichia coli (strain K-12) (Species: Escherichia coli (Species: IO:Sep-1999 #text\_change 01-Mar-2002 C; Accession: G65010; Judicali; 141200 R; Blatther, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M., A.; Rose, D.J.; Mau, B.; Shao, Y. Shao, Y. A.; Rose, D.J.; Mau, B.; Shao, Y. A.; Rose, D.J.; Mau, B.; Shao, Y. A.; Riletter complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617; PMID:9278503

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Habitation histidine kinase/response regulator [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Accession: H872 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Accession: H872 #sequence_revision 20-Apr-2001
C; Accession: H872 #sequence_revision 7.; Fallow, M.E.; Eisen, J.; Heidelberg,
C; Allow, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.E.; Eaft, D.H.; Ko
n, J.; Ermolaeva, M.; Wilte, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc.
Natl. Accession H874 #sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Accession H874 #sequence of Caulobacter crescentus.
A; Molecule type: DNA
A; Residues: 1-394 KSTO>
A; Residues: 1-394 KSTO>
A; Residues: 1-394 KSTO>
A; Genetics:
A; Genetics:
A; Genetics:
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Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: C85879
A; Astatus: preliminary
A; Molecule type: DNA
A; Residues: 1-1197 <STO>
A; Residues: 1-1197 <STO>
A; Cossreferences: GB:AE005174; NID:q12516740; PIDN:AAG57495.1; GSPDB:GN00145; UWGP: A; Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable sensor for regulator EvgA evgS [imported] - Escherichia coli (strain 0157:H7 C;Species: Escherichia coli (crain 0157:H7 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: C85879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1013 PNVDGFELTRKLREQNSSLPIWGLTANA-QANEREKGINCGMNLCLFKPLTLDVLKTHLS 1071
                                                  72 PERDGYSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                    72 PERDGYSTIKKLREMEVKSMIVGYTSLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLIN 131
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               12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM
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C;Superfamily: evgS protein; response regulator homology
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26.0%;
Best Local Similarity 34.4%;
Matches 42; Conservative 2
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           As Accession: 6050100
As factus: nucleic sound sequence not shown; translation not shown
As Residues: nucleic sound sequence not shown; translation not shown
As Residues: 11197 < CELAT>
As Cross references: GB:AE000325; GB:U000096; NID:g1788709; PIDN:AAC75429.1; PID:g1788713;
As Exercised to JIPID. January 1993
As Description: Newly identified genes involved in signal transduction of Escherichia colassication: Newly identified genes involved in signal transduction of Escherichia colassication: No. 100221
As Restaus: nucleic acid sequence not shown
As Residues: 1-151, Fr. 153-241, PL. 244-274, Rr. 276-419, FE. 422-738, 'D', 740-757, 'R', 759-87 (FESUAL) Rr. Ratayama S. Traniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Traniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Traniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Traniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Traniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Traniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Traniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Taniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Return, R.; Ratayama, S.; Taniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Ratayama, S.; Taniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Ratayama, S.; Taniguchi, M.; Horie, T.; Ikeda, M.; Tayaki, S.; Nakagawa, H.; Tayaki, S.; Nakagawa, M.; Tayaki, S.; Nakagawa, M.; Tayaki, S.; Nakagawa, M.; Tayaki, S.; Nakag
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C;Date: 18-Jul-3001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C;Accession: Agl035
R;Hayashi T:: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Aritle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Resdiues: 1.1197 - HANY>
A;Resdiues: 1.1197 - HANY>
A;Cross-references: GB:BA000007; PIDN:BAB36672.1; PID:g13362719; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
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Best Local Similarity
'hag 42; Conserv?
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G65010
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Matches
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RESULT

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A; Title: RosB and RosC: a two-component regulator of capsule synthesis in Escherichia A; Reference number: JV0068; MUID:90130299; PMID:2404948
A; Recession: JV0069
A; Molecule type: DNA
A; Residues: 1-112, 'IG', 115-918,'S', 920-933 <STO>
A; Molecule type: DNA
A; Residues: 1-112,'IG', 115-918,'S', 920-933 <STO>
A; Cross-references: GBM28242; NID:94147525
A; Experimental source: strain K12
B; Jayaratne, P.; Keenleyside, W.J.; MacLachlan, P.R.; Dodgson, C.; Whitfield, C.
J. Bacteriol. 175, 5384-5394, 1993
A; Title: Characterization of rosB and rosC from Escherichia coli 09: K30:H12 and exam
A; Reference number: A48659; MUID:9374832; PMID:8366025
A; Status: nucleic acid sequence not shown
A; Reference number: A48659
A; Status: nucleic acid sequence not shown
A; Residues: 1-112, 'IG', 'I15-299,'V', 300-759,'E', 761-873,'T', 875-921,'V', 923-931,'E', 93
A; Cross-references: GBL111272; NID:9417527; PIDN:AAA24505.1; PID:9417528
A; Cross-references: GBL111272; NID:9417527; PIDN:AAA24505.1; PID:9417528
A; Cromment: This protein acts as the sensor of the two-component regulatory system to C; Genetics:
C; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 48 min
C; Superfamily: rosC protein; response regulator homology
C; Reyconds: autrophosphorylation; capsule synthesis; phosphohistidine; phosphoprotein; F; 4-26/Domain: transmembrane #status predicted <TML>
F; 250-218/Domain: transmembrane #status predicted <TML>
F; 453/Binding site: phosphate (His) (covalent) #status predicted
F; 453/Binding site: phosphate (His) (covalent) #status predicted
F; 453/Binding site: phosphate (His) (covalent) #status predicted
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C91017,
R;Hayashi, T.: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNR Res. 8, 11-22, 2001
A;Tile: Complete genome sequence of enterohemorrhadic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Cross-references: GB:BA000007; PIDN:BAB36530.1; PID:g13362576; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
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C;Superfamily: rcsC protein; response regulator homology
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33.9%; Pred. No. 1.5e-06;
tive 32; Mismatches 37
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25.3%; Score 171.5; DB 1
Best Local Similarity 33.9%; Pred. No. 1.5e-06;
Matches 37; Conservative 32; Mismatches 37
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Best Local Similarity 33.99
Matches 37; Conservative
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A;Experimental source: strain K-12, substrain MG1655
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Nalletnate names: regulatory protein rosc
C:Species: Escherichia coli
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002
C:Accession: H64991; JV0069; A48659 Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1452, 1997
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Reference number: A64720; MUID:97426617; PMID:9278503
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                                                                                                                                                                                                       827 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNAIDIVLSDVNMPNMDGY 884
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A:Residues: 1-933 <BLAT>
                                                                                                                                                                                                                                                                                                   74 RDGVSTTKKLREMEVKSMIVGVTSLADNEE--ERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
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                                                                                                                                                       14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE
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C;Superfamily: rcsC protein; response regulator homology
C;Keywords: phosphotransferase
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       Pred. No. 3.4e-07;
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                                                                               31; Mismatches
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Bacteriol. 172, 659-669, 1990
                                           31.78;
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tes 37; Conserv
                                               Best Local Similarity
Matches 39; Conserv
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Best Loc Matches

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derobic respiration control sensor/response regulatory protein (EC 2.7.3.-) [imported c) Species: Versinia pestis
C; Species: Versinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C; Accession: AD0432
R; Parkinil, J; Wren, B. W; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. A. Parkinil, J; Wrench, B.W.; Tornin, A.; Davies, R.M.; Davies, P.; Dougan, G. II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A.Title: Genome sequence of Yersinia pestis, the Causative agent of plague.
A.Reference number: AB0001; MUID:21470413; PMID:11586350
                                                                 C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: E8764
C;Accession: E8764
E;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ernolaeva, M.; Wilter, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Nall. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; WUID:21173698; PMID:11259647
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                                  sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus
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A.Residues: 1778 «KUR»
A.Cross-references: GB.AL590842; PIDN:CAC92784.1; PID:g15981477; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.0%; Score 162.5; DB 2; Length Best Local Similarity 33.0%; Pred. No. 5.5e-06; Matches 36; Conservative 28; Mismatches 40; Indels
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Matches 33; Conservative
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A;Molecule type: DNA
A;Residues: 1-642 <STO>
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A69487
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                                                                                                                                                                                   hypothetical protein rcsC [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C.; Species: Escherichia coli (strain O157:H7, substrain EDL93 C.; Species: Escherichia coli (strain o157:H7, substrain EDL93 C.; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C.; Accession: E85861 F.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose; D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-teferences: GB: AE005174; NID: 912516556; PIDN: AAG57353.1; GSPDB: GN00145; UWGP: Z34
A; Experimental source: strain 0157: H7, substrain EDL933
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD0149
C;Accession: AD0149
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice; M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Altite: Genome sequence of Yersinia pestis, the causative agent of plaque.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Molcoule type: DNA
A;Residues: 1-957 <KUR>
A;Residues: 1-957 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC90055.1; PID:g15979276; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E85861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GVSTTKKLREMEVKSMIVGVTSLADNERERRAFMEAGLNHCLAKPLTKDKI 126
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869 RLTQRIRQLGLTLPVIGVTANALAEEKQRC-LESGMDSCLSKPVTLDVI 916
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C;Superfamily: rcsC protein; response regulator homology
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C;Superfamily: rcsC protein; response regulator homology
C;Keywords: phosphotransferase
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Best Local Similarity 27.78
Matches 39; Conservative
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A;Residues: 1-736 <HEI>
A;Cross-references: GB:AE004259; GB:AE003852; NID:g9656353; PIDN:AAF94979.1; GSFDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1831
response regulator homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Mar-2003
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Mar-2003
C;Accession: A69487
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter J.C.
A;Alitle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A;Reference number: A60250; MuID:98049343; PMID:9389475
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C.Species: Vibrio cho
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A;Residues: 1-117 <KLE>
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28.3%; Pred. No. 1.5e-06;
tive 42; Mismatches 31; Indels
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Best Local Similarity 30.8%
Matches 41; Conservative
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Best Local Similarity 28.34
Matches 36; Conservative
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V, ACCESSION: NO. 29. WOLK, C.P.; KURILZ, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Teference number: AB1807; MUDD:21595285; PMID:11759840
A;Seference number: AB1807; MUDD:21595285; PMID:11759840
A;Seference number: AB1807
A;Seferen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                two-component hybrid sensor and regulator all0729 (imported) – Nostoc sp. (strain PCC
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSF
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120 PLTKDKIIPLING 132
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ALIGNMENTS
                                                YC27_PORPU
PILH_PSEAE
ATOC_ECOLI
                                                                        YC27_GUITH
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MEDLINE-20378313; Pubmed-10923791;
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MEDLINE=93173621; PubMed*1289796;
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SEQUENCE FROM N.A.
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EVGS_ECOLI
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bacillus ha
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bordetella
bacillus me
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                                                   (without alignments)
278.071 Million cell updates/sec
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                                                                                        1 MATKSMGDIEKIKKKLNVLI.....LAKPLTKDKIIPLINQLMDA 136
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P14376
P18769
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P22763
P39928
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P48027
P96602
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P25833
P40330
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P96126
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P14375
P26275
                                            August 14, 2003, 16:46:47; Search time 23 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                              127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                             SUMMARIES
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SSK1_YEAST
GACS_PSESY
DCTR_BACSU
DCTR_BACHD
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ZRAR_ECOLI
ALGR_PSEAE
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2RAR_SALTI
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BVGS_BORBR
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CHEY_TREPA
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DCTR_BACME
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EVGS_ECO57
RCSC_SALTI
RCSC_SALTY
RCSC_ECOLI
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ARCB_ECO57
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                             protein search, using sw
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Q8x613 escherichia
P10957 escherichia
034534 bac11lus su
Q4594 caulobacter
P1644 escherichia
Q44006 alcaligenes
P49246 xanthomonas
C56312 thermotoga
P51358 porphyra pu
P43501 pseudomonas
Q0606 escherichia
O78428 guillardia
 ZRAR_ECO57
NARL_ECOLI
CITT_BACSU
CTRA_CAUCR
CPXR_ECOLI
CZCR_ALCEU
RPFC_XANCP
  25441
2226
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2231
2232
2232
120
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2461
254
  117.6
117.6
117.6
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117.3
117.0
116.6
116.6
   121.5
1119.5
1119.5
1118.5
1118.5
1115.5
1112.5
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Utsumi R., Katayama S., Ikeda M., Igaki S., Nakagawa H., Miwa A., Taniguchi M., Noda M.;
Taniguchi M., Noda M.;
"Cloning and sequence analysis of the evgAS genes involved in signal transduction of Escherichia coli K-12.";
Nucleic Acids Symp. Ser. 27:149-150(1992).
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MDDLINE-97349980; PubMed=9205837;
Yamamoto V., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kato A., Ohnishi H., Yamamoto K., Furuta E., Tanabe H., Utsumi R.; "Transcription of emrKY is regulated by the EvgA-EvgS two-component system in Escherichia coli K-12."; Biosci. Biotechnol. Biochem. 64:1203-1209(2000).
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SEQUENCE FROM N.A.
STAALN-KIZ / Mol555,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K12;

WEDLINE-94171083; PubMed-8125343;

WEDLINE-94171083; PubMed-8125343;

Utsumi R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki
Nakagawa H., Miwa A., Tanabe H., Noda M.;

"Newly identifiaed genes involved in the signal transduction of
Escherichia coli K-12.";

Gene 140:73-77(1994).
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Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (VARIANTS EVGS1 AND EVGS4).
EVGS_ECOLI STANDARD; PRT; 1197 AA. BY0855; P77644; Q9RE36; Q9RE37; 01-JUL-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FBD-2003 (Rel. 41, Last annotation update) EVGS OR B2370.
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[6]
CHARACTERIZATION.
                  (Probable)
                      domain
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DOMAIN
TRANSMEM
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EVGS_ECO57
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           MEDINE-98194702; pubmed-9535079;

Perraud A.-L., Kimmel B., Weiss V., Gross R.;

Perraud A.-L., Kimmel B., Weiss V. Gross R.;

Specificity of the Bydas and Bydas phosphorelay is mediated by the "Specificity of the Bydas procedins.";

Mol. Microbiol. 27:875-887(1998).

-!- FUNCTION: Member of the two-component regulatory system eygs/eyga.

-!- FUNCTION: Member of the two-component regulatory system eygs/eyga.

-!- FUNCTION: Member of the two-component regulatory system eygs/eyga.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamaqata S., Horiuchi T.; "Construction of a contiguous 874-kb sequence of the Escherichia coli analysis of its sequence features."; B min on the linkage map and DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp in the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002570; HbL.

InterPro; IPR001789; Response_reg.

InterPro; IPR00189; Response_reg.

InterPro; IPR001811; SBP_dlu_receptor.

InterPro; IPR00188; SBP_bac_3.

Pfam; PP00518; HisRA; I.

R PRINT; PR00497; SBP_bac_3; I.

R PRINT; PR00497; SBP_bac_3; I.

R PRINT; SM00089; HarRase_c; I.

R SMART; SM00089; HarRase_c; I.

R SMART; SM00089; HarRase_c; I.

R SMART; SM00062; PBPb; 2.

R SMART; SM00062; PBPb; 2.

R SMART; SM000649; REC; II.

R SMART; SM00062; PBPb; 2.

R SMART; SM000649; HPT; I.

R PROSITE; PS50109; HBZ, KIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SIMILARITY: Contains 1 histidine kinase domain.
-:- SIMILARITY: Contains 1 HPT domain.
-:- SIMILARITY: Contains 1 response regulatory domain.
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR005461; His_KinA.
InterPro; IPR005467; His_Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF201840; AAF17563.1; -. EMBL, AF201841; AAF17564.1; -. EMBL; AB000325; AAC75429.1; -. EMBL; D90867; BAA16241.1; -. PIR; G65010; G65010.
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122 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
102 PHOSPHORYLATION (BY SIMILARITY).
1137 F-9 S (IN EVGS1; CONSTITUTIVELY ACTIVE).
157 E->6 (IN EVGS1; CONSTITUTIVELY ACTIVE).
152 L->F (IN EVE: 1 AND 2).
243 FF->PD (IN REF. 1 AND 2).
255 W-> PD (IN REF. 1 AND 2).
275 G-> FE (IN REF. 1 AND 2).
275 G-> FE (IN REF. 1 AND 2).
276 G-> FE (IN REF. 1 AND 2).
277 SQ-> FE (IN REF. 1 AND 2).
278 G-> FO (IN REF. 1 AND 2).
279 G-> FE (IN REF. 1 AND 2).
271 C-> C (IN REF. 1 AND 2).
272 C-> FE (IN REF. 1 AND 2).
273 G-> FE (IN REF. 1 AND 2).
274 C-> C (IN REF. 1 AND 2).
275 C-> C (IN REF. 1 AND 2).
276 C-> C (IN REF. 1 AND 2).
277 C-> C (IN REF. 1 AND 2).
278 C-> C (IN REF. 1 AND 2).
279 C-> C (IN REF. 1 AND 2).
270 C-> C (IN REF. 1 AND 2).
270 C-> C (IN REF. 1 AND 2).
271 C-> C (IN REF. 1 AND 2).
272 C-> C (IN REF. 1 AND 2).
273 C-> C (IN REF. 1 AND 2).
274 C-> C (IN REF. 1 AND 2).
275 C-> C (IN REF. 1 AND 2).
275 C-> C (IN REF. 1 AND 2).
276 C-> C (IN REF. 1 AND 2).
277 C-> C (IN REF. 1 AND 2).
277 C-> C (IN REF. 1 AND 2).
278 C-> C (IN REF. 1 AND 2).
279 C-> C (IN REF. 1 AND 2).
279 C-> C (IN REF. 1 AND 2).
270 C-> C (IN REF. 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 PERDGYSTTKKLREMEVKSMIVGYTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
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STRAINE-0157:H7 / RIMD 0509952;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takani H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7, EDL933 / ATCC 700927;

MEDLINE=21074935, PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Score 178.5; DB 1; Length 1197; 34.4%; Pred. No. 2.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Indels
CYTOPLASMIC (POTENTIAL).
                                                                                RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein evgs precursor (EC 2.7.3.-).
Escherichia coli 0157:H7.
                                        HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34...
Best Local Similarity
Local A2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
        1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1045 104
1074 107
1197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1072 QL 1073
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72
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                                                                                                                                                RESULT 3
RCSC_SALTI
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                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
Res. 8:11-22(2001). FUNCTION: Member of the two-component regulatory system evgS/evgA. Phosphorylates evgA via a four-step phosphorelay in response to environmental signals (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (AUTC-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
W; A01055089D9618E2 CRC64;
                                                                                              -:- PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp in the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PSSO110, RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Signal; Complete protecme. SIGNAL 121 SENSOR PROTEIN EVGS.
CHAIN 22 1197 SENSOR PROTEIN EVGS.
DOMAIN 22 325 CYTOPLASMIC (POTENTIAL).
TRANSMEM 326 POTENTIAL.
DOMAIN 318 558 POTENTIAL.
DOMAIN 538 558 POTENTIAL.
                                                                                                                                                  domain (By similarity).
--- SMILARITY: Contains 1 histidine kinase domain.
--- SIMILARITY: Contains 1 HPT domain.
--- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.0%; Score 176.5; DB 1
34.4%; Pred. No. 4.3e-07;
tive 25; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003594; APPbind_ATPase.
InterPro; IPR003594; APPbind_ATPase.
InterPro; IPR003661; His_Kina.
InterPro; IPR003661; His_Kinase.
InterPro; IPR00367; His_Kinase.
InterPro; IPR001379; Response_reg.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR00131; SBP_bac_3.
Pfam; PF00512; HisKa; 1.
Pfam; PF00072; response_reg; 1.
Pfam; PF00072; response_reg; 1.
PRIMS; PR00344; BCTRLSENSOR.
Probom; PD000039; Response_reg; 1.
SWART; SM00039; Response_reg; 1.
SWART; SM00073; HPT; 1.
SWART; SM00073; HPT; 1.
SWART; SM00073; HPT; 1.
PROSITE; PS50044; HPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134953 MW;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE005468; AAG57495.1; -. EMBL; AP002561; BAB36672.1; -. PIR; A91035; A91035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1197
721
1009
1137
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SEQUENCE
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MOD_RES
MOD_RES
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                          1013 PNVDGFELTRKLREQNSSLPIWGLTANA-QANEREKGLNCGMNLCLFKPLTLDVLKTHLS 1071
PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=TV2 / ATCC 700931;
MEDLINE=22531377; PubMed=12644504;
MEDLINE=22531377; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity)
--- SIMILARITY: Contains 1 histidine Kinase domain.
--- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
--- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 178:1691-1698(1996).

-i. FUNCTION: Member of the two-component regulatory system rcsC/rcsB intolved in the regulation of the expression of genes involved in colanic acid capsule synthesis. RcsC probably functions as a membrane-associated protein kinase that phosphorylates rcsB in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Dougar G., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Brooks K., Chillingworth T., Connerton P., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhitehead S., Barrell B.G.; Eacher S., O'Gaora P., Parry C., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CTIB.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-TY2 / ATCC 700931, MEDLINE-96198173; PubMed-8626298; Artogeux I., Waxin H., Ecobichon C., Lee J.O., Popoff M.Y.; Yatlogeux I., Waxin H., Ecobichon C., Lee J.O., Popoff M.Y.; Characterization of the rosh and rosh genes from Salmonella typhics through twin is involved in regulation of Vi antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response to environmental signals.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                 948 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 185:2330-2337(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                       RCSC OR STY2496 OR T0594.
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                     1072 QL 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=601;
                                                                                           132 QL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Probable)
                                                                                                                                                                                                                                                                                                                                                                                  component C)
                                                                                                                                                                                                                                              RCSC_SALTI
Q56128;
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ä

3; Gaps

52; Indels

Conservative

Local Similarity es 42; Conserv

Best Loc Matches

g ò

12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71  us-09-646-679-15.rsp

Page

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  827 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNAIDIVLSDVNMPNMDGY 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              940 RESPONSE REGULATORY.

179 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

775 PHOSPHORYLATION (BY SIMILARITY).

106237 MW; AE3A21701265A865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sensory transduction; Transferase; Kinase; Bacterial capsule;
Inner membrane; Transmembrane; Phosphorylation; Complete proteome.
DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rsc (EC 2.7.3.-.) (Capsular synthesis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 948;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 173.5; DB 1; 33.9%; Pred. No. 5.9e-07; tive 33; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             948 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0109; HIS_KIN; 1.
PROSITE; PSS0112; PAS; FALSE_NEG.
PROSITE; PSS0110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                           InterPro; IPR003594; ATPbind AFPase.
InterPro; IPR004359; Bact_sens_pr_C.
InterPro; IPR003661; His_kinA.
InterPro; IPR005467; His_kinase.
InterPro; IPR000149; PAS_domain.
InterPro; IPR001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                Ffam; PF02518; HATPASS_C, 1.
Pfam; PF00512; HASKA: 1.
Pfam; PF00072; response_reg; 1.
Probom; PD000039; Response_reg; 1.
SWART; SW00348; HATPASS_C, 1.
SWART; SW00348; HATPASS_C, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                        EMBL; AE016836; AA068299.1; -.
                                                                                                                                                                                          EMBL; X87830; CAA61095.1; -. HSSP; P06143; 1UDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  948 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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P58662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        component C)
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MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
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TD RCSC_SC_SC
AC POST 28-FBB
DT 28
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STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDINE=21534948; Pubmed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille-P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IPR003594; ATPDING_ATPASE.
R InterPro; IPR003594; ATPDING_ATPASE.
R InterPro; IPR003661; His_KinA.
R InterPro; IPR003661; His_KinA.
R InterPro; IPR001789; Response_reg.
R InterPro; IPR001789; Response_reg.
R InterPro; IPR001789; Response_reg.
R Pfam; PF00512; His_Kin 1.
R Pfam; PF00512; His_Kin 1.
R Pfam; PF000139; Response_reg; 1.
R Pfam; PF000139; Response_reg; 1.
R R Propom; P000039; Response_reg; 1.
R RMART; SM00344; BCTRLSENSOR.
R SMART; SM00388; His_Kin 1.
R RARRT; SM00388; His_Kin 1.
R RROSITE; PS50110; HIS_Kin 1.
R RROSITE; PS50110; RESPONSE_REGULATORY; 1.
R ROSITE; PS50110; RESPONSE_REGULATORY; 1.
R PROSITE; PS50110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                     PTR: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).

SIMILARITY: Contains I histidine kinase domain.

SIMILARITY: Contains I PAS (PER-ARNT-SIM) dimerization domain.

SIMILARITY: Contains I response regulatory domain.
                                                                                                             940 RESPONSE REGULATORY.
479 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
875 PHOSPHORYLATION (BY SIMILARITY).
106279 MW; BAAADBDA557D5868B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Byan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

Lyoneplete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.4%; Score 172.5; DB 1; Length 948; 34.6%; Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 STIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKD 124
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Best Local S:
Matches 37
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MOD_RES
SEQUENCE
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935
949 AA;
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG10822;
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P18769;
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MOD_RES
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VARIANT
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-!- PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of rcsB and rcsC from Escherichia coli 09:K30:H12 and examination of the role of the rcs regulatory system in expression of group I capsular polysaccharides.";
J. Bacteriol. 175:5384-5394(1993).
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-!- SIMILARITY: Contains 1 histidine kinase domain.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-!- SIMILARITY: Contains 1 response regulatory domain.
-!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
SILON STRAIN=K12 / MG1655;
SILON STRAIN STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=X12;
MEDLINE=90130299; PubMed=2404948;
Stout V., Gottesman S.;
Ross and Rosc: a two-component regulator of capsule synthesis in
Escherichia coli.";
                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=562;
                                                                                  RCSC_ECOLI STANDARD; PRT; 949 AA.
P14376; P76457; P97170; P97202; Q47586;
01-3An-1990 (Rel. 13, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93374832; PubMed-8366025;
Jayaratne P., Keenleyside W.J., Maclachlan P.R., Dodgson C.,
Whitfield C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12;
MEDLINE=97251358; Pubmed=9097040;
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                                                                                                                                                                                                                                                     component C).
RCSC OR B2218.
Escherichia coli.
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RESPONSE REGULATORY.
479
PHOSPHORILATION (AUTO-) (BY SIMILARITY).
875
L-9V (IN STRAIN 09:K30:H12).
776
K-> E (IN STRAIN 09:K30:H12).
890
I -> Y (IN STRAIN 09:K30:H12).
948
D -> E (IN STRAIN 09:K30:H12).
948
D -> E (IN STRAIN 09:K30:H12).
948
T -> S (IN REF. 1 AND 2).
935
T -> S (IN REF. 1.).
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R SWART; SMOUUL,

R PROSITE; PS501109; HIS_KIN, 1.

R PROSITE; PS501109; HIS_KIN, 1.

R PROSITE; PS501109; HIS_KIN, 1.

R PROSITE; PS50110; PRAS; FALSE NEG.

DR PROSITE; PS50110; PRAS; FALSE NEG.

KW Inner membrane; Transferase; Kinase; Bacterial capsule;

KW Inner membrane; Transferase; Kinase; Posphorylation; Complete proteome.

KW Inner membrane; Transferase; Kinase; Posphorylation; Complete proteome.

FT PRANSMEM 20 41 POTENTIAL.

FT PRANSMEM 42 313 PERIPILASMIC (POTENTIAL).

FT PRANSMEM 335 CYTOPLASMIC (POTENTIAL).

AA9 CYTOPLASMIC (POTENTIAL).

AA9 CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777
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EMBL: L11272; AAA24505.1; ALT_INIT.
EMBL: A5000311; AAC7578.1; ALT_INIT.
EMBL: D90850; BAA16001.1; ALT_FRAME.
EMBL: D90850; BAA16006.1; ALT_FRAME.
EMBL: D90851; BAA16009.1; ALT_FRAME.
EMBL: D90851; BAA16009.1; ALT_FRAME.
HSSP; P06143; IUDR.
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ID FRZE_M
AC P18769
DT 01-NOV
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                                                                                                                                                                                                                                                                                                    MEDLINE=91072208; Pubmed=213853;

A MCGleary W.R., Zusman D.R.;

The Purification and characterization of the Myxococcus xanthus Frze

The Purification and characterization of the Myxococcus xanthus Frze

The Profesin shows that it has autophosphorylation activity.";

The Bacteriol. 172:6661-6668(1990).

-!- FUNCTION: FRZE IS INVOLVED IN A SINSORY TRANSDUCTION PATHWAY THAT

CONTROLS THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING

DIRECTION: FRZE SEEMS TO BE CAPABLE OF AUTOPHOSPHORYLATING ITSELF

ON AN HISTIDINE RESIDUE AND THEN TO TRANSFER THAT GROUP TO AN

ASPARTATE RESIDUE IN THE C-TERMINAL PART OF THE PROTEIN.

-!- SIMILARITY: Contains 1 histidine kinase domain.

C-!- SIMILARITY: Contains 1 histidine kinase domain.

C-!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESPONSE REGULATORY.
PROSPHORYLATION (AUTO.) (BY SIMILARITY).
ALA/PRO-RICH (POSSIBLE HINGE REGION).
9912BD40991C69E5 CRC64;
                                                                                                                                                                                                McCleary W.R., Zusman D.R.; "FrzB of Myxococus xanthus is homologous to both Chea and CheY of Salmonealla typhimurium"; Proc. Natl. Acad. Sci. U.S.A. 97:5899-5902(1990).
                                                                                         Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Kinase; Phosphorylation.
01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Gliding motility regulatory protein (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HISTIDINE KINASE.
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RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A35966; A35966.

BSSP; Q56310, BB3Q.

InterPro; IPR001594; ATPbind_ATPase.

InterPro; IPR001594; ATPbind_ATPase.

InterPro; IPR001594; CheW.

InterPro; IPR0015467; His_kinase.

InterPro; IPR001789; Response_reg.

Fam; PF01584; CheW; I.

Pfam; PF01584; CheW; I.

Pfam; PF01674; Hpt; I.

Pfam; PF01677; Hpt; I.

Pfam; PF01677; Hpt; I.

Pfam; PF01677; Hpt; I.

Pfam; PF01072; response_reg; I.

PRNNTS; PR00344; BCTRLSENSOR.

PRODAGON; PD0000193; Response_reg; I.
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                                                                                                                                                                                  MEDLINE-90332690; PubMed-2165608;
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SMART; SM00387; HATPASE_C; 1.
SMART; SM00073; HPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83189 MW;
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PS50109; HIS_KIN; 1.
PS50894: HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M35192; AAA25396.1; -.
                                                                                                                                                                                                                                                                                            PHOSPHORYLATION OF HIS-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sensory transduction;
                                                                           Myxococcus xanthus.
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50894;
PROSITE; PS50110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50851;
PROSITE; PS50109;
                                                                                                                               NCBI_TaxID=34;
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DB 1; Length 777;

23.1%; Score 156.5;

Query Match

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                     'n
                                                                                                        657 KRLRVLLVDDSPIARATEGALVKALGHSVEEAQDGEEAYV--KVQNNTYDLILTDVQMPK 714
                                                                14 KKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94042854; PubMed=8226633;
Brown J.L., North S., Bussey H.;
"SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
beta-glucan assembly, encodes a product with domains homologous to
prokaryotic two-component regulators and to heat shock transcription
factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway.";
EMBO J. 13:5186-5194(1994).
-!- FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT
-!- FUNCTION IN A TWO-COMPONENT SIGNAL TRANSDUCTION PATHWAY THAT
ACTS IN PARALLEL WITH THE PKCI CASCADE TO REGULATE GROWTH AT THE
CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2288C / AB972;
STRAIN=24378003; PubMed=8091229;
SIRDINE-54378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langaton Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Perer H., Trevaskis E., Vaughan R.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                     5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown J.L., Bussey H., Stewart R.C.; "Yeast Skn?p functions in a eukaryotic two-component regulatory
                                                                                                                                                   74 RDGVSTTKKLREMEVKSMI--VGVTSLADNEEERRAFMEAGLNHCLAK 119
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krems B., Charizanis C., Entian K.-D.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                      SKN7_YEAST STANDARD; PRT; 622 AA.
P38889; P9747;
01.FEB-1995 (Rel. 31, Created)
01.FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative transcription factor SKN7 (POS9 protein).
SKN7 OR POS9 OR BRY1 OR YHR206W.
  ilarity 35.2%; Pred. No. 1.2e-05;
Conservative 27; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 175:6908-6915(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 265:2077-2082(1994).
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Best Local Similarity
Matches 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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DOMAIN
TRANSMEM
DOMAIN
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'Genome
69 KEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI-- 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMD
         EMBL; W00485; AAC46911.1; -

DR EMBL; W00029; AAB69143.1; -

DR EMBL; W00029; AAB6914.1; -

DR EMBL; W00029; AAB6914.1; -

DR EMBL; W00029; AAB6914.1; -

DR EMBL; W000249; EMBC914.1; -

DR SGD; SG001249; SKN7.

GO; GO:0005504; C:nucleus; IDA.

GO; GO:000550; F:transcription factor activity; IDA.

GO; GO:000550; F:transcription; IDA.

GO; GO:000550; F:transcription; IDA.

GO; GO:000550; F:transcription; IDA.

InterPro; IPR001231; HSE_DNA_bind.

InterPro; IPR001241; HSE_DNA_bind.

InterPro; IPR001589; Response_reg; 1.

PROMM; PR00057; response_reg; 1.

PROMM; PR00178; PR00188; HSE_DNA_bind; 1.

PRODON; PD000198; HSE_DNA_bind; 1.

PRODON; PD000198; HSE_DNA_bind; 1.

PRODON; PS001098; HSE_DNA_LNI, 1.

PROSTIE; PS00414; HSE_DNA_IN; 1.

PROSTIE; PS00414; HSE_DNA_IN; 1.

PROSTIE; PS00414; HSE_DNA_IN; 1.

PROSTIE; PS00414; HSE_DNA_IN; 1.

PROSTIE; PS04141; HSE_DNA_IN; 1.
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STRAIN=0157:H7 / ED1933 / ATCC 700927;
STRAIN=0157:H7 / ED1933 / ATCC 700927;
STRAIN=01704935:Pubbmed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae, Escherichia.
NCBL_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Aerobic respiration control sensor protein arcB (EC 2.7.3.-).
ARCB OR Z4574 OR ECS4089.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.1%; Score 150; DB 1; Length 622;
28.1%; Pred. No. 3.3e-05;
Live 32; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                         RESPONSE REGULATORY.
PHOSPHORYLATION (PROBABLE).
D-N: DIMINISHED ACTIVITY.
4C732FD66E326742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             778 AA
                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                           427 427 PH
427 427 D-
427 427 D-
622 AA; 69202 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ----- 1PLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 ILIRYLKDRIPLCEQ 501
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Best Local Similarity 28.1
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARCB_ECO57
P58363;
                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
MUTAGEN
MUTAGEN
SEQUENCE
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DOMAIN
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Natice of Seguence of Contectohemorrhapic Escherichia coll 0157;H7.";

Natice 000529-531(2001).

Natice 00529-531(2001).

Natice 00529-531(2001).
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SPECIES=E.coli; STRAIN=M15;

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584 GLDISRELTKRYPREDLPPLVALTANVLKDKQEYLNAGMDDVLSKPLSVPALTAMIKKFW 643
                                                                                                                                                                                                                                                                                                                                                                                                            75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                            16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GVSTTKKLREMEVKSMIVGVTSLADNE-EERRAFMEAGLNHCLAKPLTKDKIIPLINQLM
                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
CHARDOLEDOY CROC4;
CHARDOLEDOY CROC4;
                                                                                                                                                                                                                                                                                                                                                      Gaps
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SEQUENCE FROM N.A.
SPECIES-E coli; STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riathy M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=562, 623;
                                                                                                                                                                                                                                                                                    22.1%; Score 149.5; DB 1; Length 778; 25.6%; Pred. No. 4.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG'1991 (Rel. 19, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acrobic respiration control sensor protein arcB (EC 2.7.3.-).
ARCB OR B310 OR SF3250.
Escherichia coli, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                     HISTIDINE KINASE.
RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               778 AA
                                                                                                                                                                                                                                                                                                                                                   40; Mismatches
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                                                                                                                                                                                                                                    88010 MW;
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                                                                                                                                                                                                                                 778 AA;
                                                                                                                                                                                                                                                                                                                             Similarity
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153
226
2289
289
527
578
576
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Best Local S.
Matches 31
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acta Crystallogr. D 55:1842-1849(1999).

Acta Crystallogr. D 55:1842-1849(1999).

-!- FUNCTION: Member of the two-component regulatory system arcB/arcA.

Sensor-regulator protein for anaerobic repression of the arc
modulon. Activates arcA via a four-step phosphorelay. ArcB can
also dephosphorylate arcA by a reverse phosphorelay involving His-
717 and Asp-576.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                        SPECIES=E.Coli, STRAIN=M15;
MEDLINE-99047671; PubMed-9830034;
Georgellis D., Kwon O., De Whif P., Lin E.C.C.;
"Signal decay through a reverse phosphorelay in the arc two-component signal transduction system";
J. Biol. Chem. 273:32864-32869(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WITH CHEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kato M., Mizuno T., Hakoshima T.;
"Crystallization of a complex between a novel C-terminal transmitter,
HPt domain, of the anaerobic sensor kinase ArcB and the chemotaxis
response regulator Chey.";
Acta Crystallogr. D 54:140-142(1998).
                                                                                                                                                                                                                                                                                                                                                                         by the arc two-component system of Escherichia coli."; J. Bacteriol. 182:3858-3862(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HPt)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-E.coli;
MEDLINE-20003135; PubMed=10531481;
Atto M., Mizuno T., Shimizu T., Hakoshima T.;
"Refined structure of the histidine-containing-phosphotransfer (HPt) domain of the anaerobic sensor kinase ArcB from Escherichia coli at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS) OF 660-778.
SPECIES-E.coli
MEDLINE-97207018; PubMed-9054511;
MELO M. Mizuno T., Shimizu T., Hakoshima T.;
"Insights into multistep phosphorelay from the crystal structure of the C-terminal HPt domain of ArcB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OUMLAIN.
-!- SIMILARITY: Contains 1 histidine kinase domain.
-!- SIMILARITY: Contains 1 HPT domain.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
-!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group from a His in the primary transmitter domain, to an Asp the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Probable).
PTM: Activation requires a sequential transfer of a phosphate
    MEDLINE-97431492; PubMed-9286997;
Georgellis D., Lynch A.S., Lin E.C.C.;
"In vitro phosphorylation study of the arc two-component signal
transduction system of Escherichia coli.";
J. Bacteriol. 179:5429-5435(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 659-776 IN COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS) OF 659-776
                                                                                                                                                                                                                                                                                                        HIS-717
                                                                                                                                                                                                                                                                                                                              SPECIES-E.coli, STRAIN-K12 / MC4100;
MEDLINE-20109722; PubMed=10851007;
Kwon O., Georgellis D., Lin E.C.C.;
Phosphorelay as the sole physiological
                                                                                                                                                                                                                                                                                                          MUTAGENESIS OF HIS-292; ASP-576 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli;
MEDLINE=98437504; PubMed=9761838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 88:717-723(1997)
                                                                                                                                           CHARACTERIZATION.
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SLN1_YEAST
ID SLN1_YEAST
AC P39928;
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                                                                                                                                                                       ECOGENE; EGLUUDZ; arCB.

BR InterPro: IPR00354; ArDbind_ATPase.

BR InterPro: IPR00354; ArDbind_ATPase.

BR InterPro: IPR003561; His_Kinase.

BR InterPro: IPR002570; Hts_Kinase.

BR InterPro: IPR0001700; PAS-assoc_C.

BR InterPro: IPR0001700; PAS-assoc_C.

BR InterPro: IPR0001700; PAS-assoc_C.

BR InterPro: IPR000170; PAS-assoc_C.

BR PR00012; PAS-i.

BR MART; SM00039; Response_reg; 1.

BR SMART; SM00039; RESponse_reg; 1.

BR SMART; SM00041; PAS: 1.

BR SMART; SM00041; PAS: 1.

BR SMART; SM00041; PAS: 1.

BR PROSITE; PS50109; HFF; 1.

BR PROSITE; PS50109; HFF; 1.

BR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

BR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

BR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

BR PROSITE; PS50110; Transferase; Kinase; Phosphorylation; 3D-structure; MW Transmembrane; Inner membrane; Iranscenting and Armany and A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-).
PHOSPHORYLATION (PROBABLE).
PHOSPHORYLATION (PROBABLE).
H->Q: LOSS OF ACTIVITY.
D->A: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels
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DD61EA6ECF95AD30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
PERIPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISTIDINE KINASE.
RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.1%; Score 149.5; DB 1
25.6%; Pred. No. 4.6e-05;
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X53315; CAA37397.1; -.
U18997; AAA58012.1; -.
AE000400; AAC76242.1; -.
AE015336; AAN44715.1; -.
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                                                                                          PDB: 1A0B: 18-MAR-98.
PDB: 2A0B: 17-JUN-98.
PDB: 1BDJ: 11-MAY-99.
PDB: 1FR0: 31-DEC-02.
ECOGENE: EG10062; arcB
                                                                          PIR; D65112; RGECAR.
PDB; 1A0B; 18-MAR-98
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CONFLICT
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MOD_RES
MOD_RES
MUTAGEN
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Matches
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DESIGNATION PRINCES AND PRINCE
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GACS_PSESY
P48027;
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                        RESPONSE REGULATORY.
PHOSPHORYLATION (ATTO.) (PROBABLE).
PHOSPHORYLATION (ATTO.) (PROBABLE).
N-LINKED (GLCNAC...) (POTENTIAL).
H->O: INACTIVE.
G->D: SLOW GROWTH, SLN1-1 MUTANT.
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SEQUENCE FROM N.A., AND MUTAGENESIS.
MEDILNE-94239498; PubMed-8183345;
Maeda T., Wurgler-Murphy S.M., Saito H.;
Maccomponent system that regulates an osmosensing MAP kinase
cascade in yeast.";
Nature 369:242-245(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomyceteles; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.4%; Score 145; DB 1; Length 1220; 29.0%; Pred. No. 0.00018;
                                                                                                                                                           PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134434 MW; 45FFE24A8165486B CRC64;
                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                             HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Mismatches
Pfam; PF00518; HATPASe_c; 1.
Pfam; PF00512; HiskR: 1.
Pfam; PF00072; response_reg; 1.
PRINTS; PR0034; BCTRLERNSOR.
Probom; PD000039; Response_reg; 1.
SMART; SM00387; HATPASe_c; 1.
SMART; SM00388; HiskR: 1.
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MEDLINE=97313267; PubMed=9169871;
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Best Local Similarity
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CARBOHYD
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MUTAGEN
SEQUENCE
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TRANSMEM
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EMBL; Z73178; CAA97528.1; -.
EMBL; Z73178; CAA97528.1; -.
SGD; S0001996; SSK1.
GO; GO:0007234; P:response to hydrogen peroxide; IMP.
InterPro; IPR001789; Response_reg; I.
From; PF000772; response_reg; I.
SMART; SM00448; REC; P.
SMART; SM00448; REC; P.
SMART; SM00448; REC; P.
SMART; SM00449; REC; P.
SMART; SM00440; RESPONSE_REGULATORY; I.
SMART; SM00440; RESPONSE_REGULATORY; I.
Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Louis E.J., Messenguy F., Meyes H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Wueller-Auer S., Nentwich U., Obermaier B., Rieger M., Rinke M., Scherens B., Scholler P., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Verendeels F., Voet M., Volckaert G., Voss H., Wamburt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.", Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.2%; Score 143.5; DB 1; Length 712; 27.9%; Pred. No. 0.00013; live 28; Mismatches 42; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (PROBABLE).
D-N: ACTIVATES.
P -> S (IN REF. 1).
33B2DBB4FCF2528A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESPONSE REGULATORY
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01-FEB-1996 (Rel. 33, Last sequence update)
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Best Local Similarity 27.9
Matches 39; Conservative
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554
181
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712 AA;
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MEDLINE-98044033; PubMed-9384377;
284 PH
707 PH
853 PH
99195 MW;
                                                   Query Match
Best Local Similarity 27.uv
The 35, Conservative
THE
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                       124 DKIIPLI 130
                                                                                                                                                                                                                                       167 RQLAQVV 773
284
707
853
907 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                               DCTR_BACSU
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                       RESULT 13
DCTR_BACSU
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    FT
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                                                                                                                                                                        regulátors.";
J. Bacteriol. 174:3011-3020(1992).
J. Bacteriol. FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
-!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
GACA/GACS(LENA). MAY BE INVOLVED IN LESION FORMATION, SWARMING AND
IN THE PRODUCTION OF EXTRACELLULAR PROTEASE, SYRINGOMYCIN AND N-
ACYL-L-HOMOSERINE LACTONE (ACYL-HSL). REQUIRED FOR PATHOGENICITY
                                                                                                                                                                                                                                                                                     -i.viruscuria.

PTM: Activation requires a sequential transfer of a phosphate group from a H1s in the primary transmitter domain, to an Asp in the receiver domain and to a H1s in the secondary transmitter domain (By similarity).

-i. SIMILARITY: Contains 1 HAMP domain.

-i. SIMILARITY: Contains 1 Histidine kinase domain.

-i. SIMILARITY: Contains 1 HPT domain.

-i. SIMILARITY: Contains 1 HPT domain.
                                                                                                                    MEDLINE-92234961; PubMed-1314807;
Hrabak E.M., Willis D.K.;
"The lemA gene required for pathogenicity of Pseudomonas syringae pv.
syringae on bean is a member of a family of two-component
                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                           Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMART; SMU448; REC; 1.
PROSITE; PS50885; HAMP. 1.
PROSITE; PS50894; HPT; 1.
PROSITE; PS50194; HPT; 1.
PROSITE; PS50110; RSPONSE_REGULATORY; 1.
Sensory transduction; Fransferase; Kinase; Phosphorylation; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
HAMP.
HISTIDINE KINASE.
RESPONSE REGULATORY.
HPT.
        Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004589; Bact_Sens_Dr_C.
InterPro; IPR004560; HAMP.
InterPro; IPR003660; HAMP.
InterPro; IPR003660; His_kina.
InterPro; IPR003667; His_kinase.
InterPro; IPR001789; Response_reg.
Fram; PF00572; HAMP; 1.
Pfam; PF00512; HAMP; 1.
Pfam; PF00512; HAMP; 1.
Pfam; PF00512; HAMP; 1.
Pfam; PF00512; HSKA; 1.
Pfam; PF00512; HSKA; 1.
Pfam; PF00512; HSKA; 1.
Pfam; PF00514; BCTRLSENSOR.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00384; HAMP; 1.
SMART; SM00386; HisKA; 1.
SMART; SM00386; HisKA; 1.
SMART; SM0073; HPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro, IPR003594, ATPbind_ATPase.
Interpro, IPR004358, Bact_sens_pr_C.
               Sensor protein gacs (EC 2.7.3.-). GACS OR LEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M80477; AAA25877.1; -.
HSSP; P06143; 1UDR.
                                                                                                         SEQUENCE FROM N.A.
        28-FEB-2003 (Rel.
                                                                                  NCBI_TaxID=321;
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TRANSMEM
TRANSMEM
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DOMAIN
DOMAIN
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REAL KURDELNE-98444077;
RADELNE-9844403; PubMed-9584377;
RADELNE-9844403; PubMed-9584977;
RA Arevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Arevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Bouriser L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Burschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.P., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.P., Cummings N.J., Daniel R.A.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henut A.,
RA Hilbert H., Hölsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Eolsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Murita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Portetelle D., Porwollik S., Perscott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Rey M., Reynolds S.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Sadate Y.,
RA Rieger M., Tamakoshi A., Taraka A., Serror P., Shin B.S., Soldo B.,
RA Rosarchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Hoster P., Wilpat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata R.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 KEMPERDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGG-----SSFDLILMD
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
5B974665DAF3492C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.; "A 148 kbp sequence of the region between 35 and 47 degree of the Bacillus subtilis genome."; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       20.9%; Score 142; DB 1; Length 907; 27.6%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p96602; P94503;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable C4-dicarboxylate response regulator dctR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 AA
                                                                                                                                                                                                                                                                                                                     33; Mismatches
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Probable C4-dicarboxylate response regulator dctR.
DCTR OR BH2751.
                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemotaxis protein cher homolog CHEY OR CHEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP001516; BAB06470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 29.49
Matches 35; Conservative
                                                                                  Bacteria; Firmicutes;
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=168 / OI1085;
                                                                   Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
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DNA_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 RKEWKVLLIEDDPMVQEVNKDFITTYKGVTVCATAGNGEBGMKLIKE--EQPDLVILDVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 KKKLNVLIVDDDPLNLIHEKIIKAIGGIS--QTANNGEEAVIIHRDGGSSFDLILMDKE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                 Asai K., Baik S.-H., Kasahara Y., Moriya S., Ogasawara N.;
"Regulation of the transport system for C4-dicarboxylic acids in Bacillus subtlis."
Microbiology 146:263-271(2000).
-I. FUNCITON: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 MPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MPKKDGIKTLQEIRKQKLEVDVI-VVSAAKDKETISIMLQNGAVDYILKFFKLERM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
               complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.7%; Score 140.5; DB 1; Length 226; 25.9%; Pred. No. 6.7e-05; Live 39; Mismatches 42; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY).
H-T-H MOTIE (POTENTIAL).
F - I (IN REF. 3).
018115514E9EF47D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transcription regulation; DNA-binding; Activator; Phosphorylation; Complete proteome.

DOMAIN 13 123 RESPONSE REGULATORY.
                                                                                                                                                                                                      Morel-Deville F., Ehrlich S.D., Morel P., "Identification by PCR of genes encoding multiple response requiators.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-1- PTM: PHOSPHORYLATED BY DCTS (PROBABLE).
-1- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB001488; BAA19283; 1; EMBL; 299106; CAB12253; 1; EMBL; 082809; AB41751.1; PIR; B69771; B69771; B69771; B69771; B61771; B61771; B7177; B
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20170658; PubMed-10708364; Asai K., Baik S.-H. Karahara
                                                                                                                                                                                   MEDLINE=97311990; PubMed=9168601;
                                                                                                                                                                                                                                                                                                    Microbiology 143:1513-1520(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 206 H
24 24 F
226 AA; 25539 MW;
                                                                                                                                   SEQUENCE OF 14-101 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                      Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND GENE NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCTR_BACHD
Q9K998;
                                                                                                                                                                                                                                                                                     regulators.
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DNA_BIND
CONFLICT
SEQUENCE
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DCTR_BACHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LNVLIVDDDPLNLIIHEKIIKAIGG--ISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 RDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 IRVLLIEDDPMVQEVNRMFVEXLSGFTIVGTTATGEEGMVKTRE--LQPDLILLDIFMPK
                                                                                                                                                                                                                                            Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ņ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 59 PHOSPHORYLATION (BY SIMILARITY).
183 209 H-T-H MOTIF (POTENTIAL).
230 AA; 26376 MW; 06FD65F46FC57D40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P10977; IRML.
HSSP, P10977; IRML.
HSSP, P10977; IRML.
Pfam; PF00072; response_reg; 1.
PIRSP PREFOOGI11; RR_cltrat_malat; 1.
PIRSP; PIRSPOOGI11; RR_cltrat_malat; 1.
SMART; SM00448; REC; 1.
SMART; SM00448; REC; 1.
PROSITE; PSSO110; RESPONSE_REGULATORY; 1.
PROSITE; PSSO110; RESPONSE_REGULATORY; 1.
Activator; Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423;
Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESPONSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.7%; Score 140.5; DB 1
29.4%; Pred. No. 6.9e-05;
Live 32; Mismatches 47
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CHEY_BACSU
P24072: P37883;
CHE4072: P37883;
C1-MAR-1992 (Rel. 21, Created)
O1-CAT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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64

DA PE

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Search completed: August 14, 2003, 16:47:19
Job time : 24 secs
                                                                                                                                                          EWBL; M59781; AAA22311.1; -.
EMBL; 299112; CAB13506.1; -.
EMBL; M66738; AAA22450.1; -.
PIR; A40874; AAA2451.1; -.
PIR; A40874; A40874.
HSSP; Q56312; 1TMY.
Subfilist; BG10258; cheY.
InterPro: IPRO01789; Response_reg; PFan; PRO0072; response_reg; 1.
ProDom; PD000039; Response_reg; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                    RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Broinlet S., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Karamata D., Kasahara Y., Klein C., Makis G., Kooris B., Karamata D., Kasahara Y., Klein C., RA Kootter P., Koningstein G., Krogh S., Kumano M.,
RA Kunita K., Lapidus A., Liu H., Masuda S., Mamel C., Mediauc C.,
RA Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Median N., Pohl T.M., Portetelle D., Porwollik S., Rey M., Reynolds S.,
RA Satro T., Sekowaka A., Secha B., Rose M., Sadale Y.,
RA Schilu C., Tackabash H., Takemash H., Takemaru K.,
RA Schilu G., Rocha E., Roche B., Rose M., Sadale Y.,
RA Schilu M., Tamakoshi B., Takapishi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanamochi M., Vannier F., Vassanotti A.,
RA Voshida K., Voshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA The complete genome sequence of the Gram-positive bacterium Bacillus
RH The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93078625; PubMed=1447979;
Bischoff D.S., Ordal G.W.;
"Identification and characterization of Flix, a novel component of
the Bacillus subtilis flagellar switch complex.";
Mol. Microbiol. 6:2715-2723(1992).
                            Bischoff D.S., Ordal G.W.; "Sequence and characterization of Bacillus subtilis CheB, a homolog of Escherichia coli CheY, and its role in a different mechanism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92283757; PubMed=1597417;
Bischoff D.S., Weinreich M.D., Ordal G.W.;
"Nucleotide sequences of Bacillus subtilis flagellar biosynthetic
genes filt and filt and identification of a novel flagellar gene,
filt.";
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STRAIN=168 / JH642;
MEDLINE=96345629;
MEDLINE=96345629;
MEDLINE=96345629;
MISSION P., Schroeder K., Schmid R., Marahiel M.A.;
Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
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J. Bacteriol. 178:4611-4619(1996).
I. PUNCTION: HAS A CENTRAL CONTROLLING ROLE IN CHEMOTAXIS.
II IS HOMOLOGOUS TO THE CHEY PROTEIN OF OTHER BACTERIA,
THOUGHT TO FUNCTION IN A DIFFERENT MANNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                      Biol. Chem. 266:12301-12305(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 174:4017-4025(1992)
                                                                                                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
      MEDLINE=91286247; PubMed=1905718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 95-119 FROM N.A.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VLIVDDDP-LNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 VSTTKKLREMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPLTKDKIIPLINQLMD 135
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62 ITALKEIKQIDAQARIIMCSAMGQSNVIDA-IQAGAKDFIVKPFQADRVLEAINKTLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50110; RESPONSE_REGULATORY: 1.
Chemotaxis; Sensory transduction; Phosphorylation; Complete proteome.
INIT_MET 0 0 0
DOMAIN 1 118
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1 118 RESPONSE REGULATORY.
53 53 PHOSPHORYLATION (BY SIMILARITY).
119 AA; 13178 MW; F3BCAOF02CAB7531 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.8%; Score 134; DB 1; Length 119; 26.9%; Pred. No. 0.00012;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 14, 2003, 16:46:47; Search time 95 Seconds (without alignments) 369.423 Million cell updates/sec

Title: US-09-646-679-15
Perfect score: 678
Sequence: 1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\* SPTREMBL\_23:\*

1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: Sp\_mammal:\*
7: Sp\_mho:\* sp\_bacteriap:\*
sp\_archeap:\* sp\_organelle:\* sp\_phage:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1		æ				
NO.	Score	Match	Query Match Length DB	DB	ID	Description
7	678	100.0	136	10	082445	082445 brassica na
7	538	79.4	142	10	Q9M8Y4	09m8v4 arabidopsis
٣	181	26.7	1969	ហ	015763	015763 dictyosteli
4	179.5	26.5	820	16	Q8EZ63	O8ez63 leptospira
ເກ	178.5	26.3	1197	16	Q8CVU5	O8cvu5 escherichia
φ	174	25.7	394	16	Q9A3P0	09a3p0 caulobacter
7	173.5	25.6	949	16	Q8FFP9	Q8ffp9 escherichia
∞	173	25.5	417	N	Q9RLC7	Q9rlc7 pseudomonas
σ	171.5	25.3	933	16	Q8XE39	O8xe39 escherichia
10	171.5	25,3	957	16	Q8ZGR4	Q8zqr4 yersinia pe
11	171	25.2	927	7	Q9ANY0	OganyO vibrio fisc
12	170	25.1	769	16	Q8PQ37	08pg37 xanthomonas
13	167.5	24.7	1364	16	Q8PJN8	08pin8 xanthomonas
14	166.5	24.6	507	7	085663	085663 proteus mir
15	163.5	24.1	1364	5₹	08883	Q8p883 xanthomonas
16	162.5	24.0	642	16	09A3L2	09a312 caulobacter

	" 4 T" E > " " 4
Q9P896 Q8ZB69 Q8ZB69 Q8ZB62 Q9GTU0 Q9GTU0 Q8D919 Q8D919 Q8D810 Q8XYW3 Q8NYQ2 Q9XXU6 Q9XXQ0 Q9XQ0 Q9XQ0 Q9AC1 Q9AC1 Q9AC1 Q9AC1	09KS16 09AS13 09A472 09A472 08KWS5 08KWS5 08KWS5 08KWS5 08KWS5 08KWS5 08KWS5 08BS7 08BS7 08BS02 08BMS3
110 110 110 110 110 110 110 110 110 110	10 10 10 10 10 10 10 10 10 10 10 10 10 1
719 1769 1769 1769 1769 176 117 117 117 126 1000 1000 1261 122	572 708 848 848 713 939 1268 120 514 929 935
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## ALIGNMENTS

RESULT 082445	1	
Π	O82445 PRELIMINARY; PRT; 136 AA.	
AC		
ď	(TrEMBLrel.	
ď	(TrEMBLrel. 08,	
Ы		
DE	Response regulator protein.	
SO	Brassica napus (Rape).	
8	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
ပ္ပ	Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae,	
ပ္ပ	eurosids II; Brassicales; Brassicaceae; Brassica.	
ŏ	NCBI_TAXID=3708;	
RN	(1)	
RP	SEQUENCE FROM N.A.	
RA	Whitelaw C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;	
RŢ	"A mRNA encoding a response regulator protein from Brassica napus is	
RT		
RL	Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AF057027; AAC62225.1;	
DR	InterPro; IPR001789; Response_reg.	
DR	Pfam; PF00072; response_reg; 1.	
DR	ProDom; PD000039; Response_reg; 1.	
DR	SMART; SM00448; REC; 1.	
DR	PROSITE; PS50110; RESPONSE_REGULATORY; 1.	
ΚW	ylation; Sensory transduction.	
SO	SEQUENCE 136 AA; 15055 MW; DA99B768FAB3CFF5 CRC64;	
ō	100.08;	
Be	Best Local Similarity 100.0%; Pred, No. 4.7e-52; Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps	0
Qy		09
qq	1 MATKSMGDIEKIKKKLNVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGS 6	09
ò	61 SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP 1	120
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QQ		120

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SEQUENCE
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
Lin X. Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Roman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC TGK12 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome annotation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.4%; Score 538; DB 10; Length 142; Best Local Similarity 78.9%; Pred. No. 9.8e-40; Matches 112; Conservative 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative response regulator protein (receiver component).
16K12.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC016829; AR726786.1;
EMBL; AY086538; AAR6269.1;
InterPro; IPR001789; Response_reg.
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Probon: PD000039; Response_reg; 1.
PROSTIE: PS50110; RESPONSE_REGULATORY; 1.
PROSTIE: PS50110; Sensory transduction.
SEQUENCE 142 AA; 15792 MW; 57487135FF2D5238 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015763 PRELIMINARY; PRT; 1969 AA.
015763 (TEMBLEL. 05, Created)
01-JAN-1998 (TEMBLEL. 05, Last sequence update)
                                                                                                                                                                                                               142 AA.
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                                   121 LTKDKIIPLINQLMDA 136
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Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                               PRELIMINARY;
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70 EMPERDGVSTTKKLREMEVKSMI-----VGVTSLADNE--EERRAFMEAGLNHCL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.7%; Score 181; DB 5; Length 1969;
35.8%; Pred. No. 5.1e-07;
ive 29; Mismatches 39; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A MEDLINE-SEARSHY; FURMENDENCY, AND ALLINE-SEARSHY; FURMENDENCY, AND ALLINE-SEARSHY; FURMENDENCY, AND ALLINE-SEARSHY; FURMENDENCY, AND ALLINE-SEARSHY; FURMENDENCY, AND ALLINE AFOLDSON, AND ALLINE AFOLDSON, AND ALLINE AFOLDSON, AND ALLINE, AFOLDSON, AND ALLINE, AFOLDSON, AND ALLINE, AFOLDSON, AND ALLINE, A
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NCBI_TaxID=173;
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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SEQUENCE 1969 AA; 219025 MW; 8E7A7952AB1BB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AE011554; AAN51193.1; -Complete proteome. SEQUENCE 820 AA; 94325 MW; 3DBE99966794R67n CPC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Two-component hybrid sensor and regulator.
LA3996.
                                                                                                                                            ictyostelium discoideum (Slime mold).
Jkaryota; Mycetozoa; Dictyosteliida; Dictyostelium
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hybrid histidine kinase DHKB.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98248997; PubMed=9576830;
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1951 QKPIKTSDILIQMI 1964
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Best Local Similarity 35.8'
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 SLL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; CC3162; -
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                                                                                                                                              63 DLILMDKEMPERDGVSTTKKLREMEVKS---MIVGVTSLADNEEERRAFMEAGLNHCLAK 119
                                                                                                                                                                                                                                                         737 DIILMDIHMPEVDGIEATKWIRSKNQNSEFPIIIALTADA-IESSKEKYISKGMNDCLTK 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71
                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     955 LPEKLSILIADDHPTNRLLLKRQLNLLGYDVDEATDGVQA--LHKVSMQHYDLLITDVNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERFAUNCE (HI / CET073 / Arcc 700928;

MEDLINE=2288624; Pubmed=12471157;

MEDLINE=288624; Pubmed=12471157;

MEDLINE=288624; Pubmed=12471157;

Rasko D., Buckles L., Liou S.-R., Boutin A., Hackett J., Stroud D., Hasko D., Buckles L., Liou S.-R., Boutin A., Hackett J., Stroud D., Hayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U. S.A. 99:17020-17024 (2002).
                                                                                                                  8 DIEK----IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSF
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia,
NCBL_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.3%; Score 178.5; DB 16; Length 1197; 34.4%; Pred. No. 4.6e-07; Live 25; Mismatches 52; Indels 3;
                                                                     15;
                      DB 16; Length 820;
                                                                   49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase, Complete proteome.
SEQUENCE 1197 AA; 134847 MW; 5088214E7F834F06 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Sensor histidine kinase/response regulator.
CC3162.
Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Sensor protein evgS precursor (EC 2.7.3.-).
                   Query Match 26.5%; Score 179.5; DB 1
Best Local Similarity 31.6%; Pred. No. 2.4e-07;
Matches 43; Conservative 29; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 AA.
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                                                                                                                                                                                                                                                                                                      120 PLTKDKIIPLINQLMD 135
                                                                                                                                                                                                                                                                                                                                                     796 PLD----LPILKSTLD 807
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les 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli 06.
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SEQUENCE FROM N.A.
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Q9A3P0;
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09A3P0
ID 09A3P1
AC 09A3P1
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262 RSAHILIVDDNATNRMVAEALCDMFECTSEQAVDGVEAVEMARSG--RFDLILMDIKMPR 319
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CONTRIBE STRONG N.C.

CARACH N.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=06:HI / CFT073 / ATCC 700928;
MEDLINE=2238024; PubMed=12471157;
MEICH RA., BURIAND V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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Enterobacteriaceae, Escherichia.
NCBL_TaxID=217992;
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PROSITE; PSS01101; RESPONSE_REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction; Complete proteome.
SEQUENCE 394 AA; 41592 MW; 6D9AF0B278B70E70 CRC64;
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sensor protein rcsC (EC 2.7.3.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR005467; His kinase.
InterPro; IPR001789; Response_reg.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF0072; response_reg; 1.
SMART; SM0039; Response_reg; 1.
SMART; SM00448; REC; 1.
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Kinase; Complete proteome
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                           SEQUENCE FROM N.A.
                             NCBI_TaxID=83334;
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Q8ZGR4
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                                                                                                                                                                      17 NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 VSTIKKLREMEVKS-----MIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                       Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sentoration update)
Sensor for ctr capsule biosynthesis, probable histidine kinase acting on RcsB.
RCSC OR 2477 B.
RCSC OR 2477 B.
RSCA CR 2477 B.
RSCA CR 2477 B.
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8
                                                                                                                                                                                                               77 VSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                             Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                            DB 16; Length 949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grandper S., Wackernagel W.;
Grandper S., Anzernagel W.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Anzugy741; Cab564741; -.
InterPro; IPR002570; Hpt.
InterPro; IPR001789; Response_reg.
                                                  e; Complete protecme.
949 AA; 106590 MW; DF8CA47F9EEB4088 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 1 1 1 SEQUENCE 417 AA, 45749 MW; D196B4FFDDA23BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                0.1-May-2000 (TrEMBLrel. 13, Created)
0.1-May-2000 (TrEMBLrel. 13, Last sequence update)
0.1-Crace 2002 (TrEMBLrel. 22, Last annotation update)
putative histidine kinase (Fragment).
of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016763; AAN81215.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.5%; Score 173; DB 2; 32.8%; Pred. No. 4e-07;
                                                                                         25.6%; Score 173.5; DB 10
33.6%; Pred. No. 9.7e-07;
iive 35; Mismatches 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction.
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                                                                                                                                                                                                                                                                                                                        417 AA
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                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00072; response_reg; I.
ProDom; P0000039; Response_reg; I.
SMART; SMO073; HPT; I.
SMART; SM00448; REC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 32.8%
les 39, Conservative
                                                                                                                           37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                             Query Match
Best Local Similarity
Matches 37; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                  Transferase;
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Q9RLC7
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1D Q6
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18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21156231; PubMed-11258796;
MEDLINE-21156231; PubMed-11258796;
Hayachi T., Makino K., Ohnishin M., Kurokawa K., Ishii K., Yokoyama K.,
Hayachi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001)
EMBL; AR004544 AAG57353.1;
ESMBL; AP002560; BAB36530.1;
HSSP; P06143; 1D42.
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                                                                                                                                                                   STRAIN—5157:H7 EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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01-MRR-2002 (TrEMBLIEL 20, Last sequence update)
01-MRR-2003 (TrEMBLIEL 23, Last annotation update)
101-MR 2003 (TrEMBLIEL 23, Last annotation update)
101-MR 2003 (TrEMBLIEL 23, Last annotation protein RcsC Treconforment sensor kinase/response regulator protein RcsC Treconformer Formation (FC 27.73.) (Sensor for ctr capsule biosynthesis).
101-MRCSC OR YPO1217 OR Y2971.
101-MRCSC ASTONIA PROTEIN OR Y2971.
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33.9%; Pred. No. 1.4e-06;
.ive 32; Mismatches 37; Indels
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PROSITE; PS50110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR003661; His_Kina.
InterPro; IPR005467; His_Kinase.
InterPro; IPR00189; Response_reg.
Fam; PF00518; Harpase_C; 1.
Pfam; PF00512; HisKA; I.
Pfam; PF0072; response_reg; 1.
Prim; PF0072; response_reg; 1.
PRINTS; PR00344; BCTRLSENSOR.
ProDom; PR00039; Response_reg; 1.
SWART; SW00388; HisKA; I.
SWART; SW00388; HisKA; I.
SWART; SW00488; HisKA; I.
SWART; SW00488; HisKA; I.
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
MEDLINE-21142508; PubMed-11208780;
                                                                                                                                                                                                                                 EMBL; AF319618; AAG60694.1;
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les 43; Conservative
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SIRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                              PERMINE-21470413; Pubbad-11586360; ParkINE-21470413; Pubbad-11586360; ParkINE-21470413; Pubbad-11586360; ParkINI J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chilingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Nature 413:523-527(2001).
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          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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L J. Bacteriol. 184:4601-4611(2002).
R EMBL; Ad41417; CAC90055.1;
R EMBL; AD01389; AAM86522.1;
R HSSP; P06143; 1D42.
R InterPro: IPR003594; ATPbind_ATPase.
R InterPro: IPR003594; ATPbind_ATPase.
R InterPro: IPR003561; His_KinA.
R InterPro: IPR003761; His_KinA.
R InterPro: IPR003761; His_KinA.
R InterPro: IPR001789; Response_reg.
R Pfam; PF0518; HATPase_c: 1.
R Pfam; PF0512; HisKA; 1.
R Pfam; PF00312; HisKA; 1.
R Pfam; PF00312; HisKA; 1.
R Pfam; PF00312; HisKA; 1.
R PROSITE; PS50109; HIS_KIN; 1.
R PROSITE; PS50109; HIS_KIN; 1.
R RAGARE; TARASELASE. Complete Proteome.
SEQUENCE 957 AA; 108591 MW; 0447AllF59100011 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                          Enterobacteriaceae; Yersinia
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SEQUENCE FROM N.A.
                                                                                                                                             SEQUENCE FROM N.A.
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                                                                          NCBI_TaxID=632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.2%; Score 171; DB 2; Length 927;
33.9%; Pred. No. 1.6e-06;
Live 28; Mismatches 42; Indels 14; Gaps
Visick K.L., Skoufos L.M.;
"A two-component sensor required for normal symbiotic colonization of Euprymna scolopes by Vibrio fischeri.";
"Bacteriol. 183:885-84(2001).
                                                      --- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cr-2002 (TrEMBLrel. 22, Created)
01-0cr-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
10-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1Wo-component system sensor protein.
1MAC0494.
1MAR-100-0s (pv. citri).
1MAR-10-0s (pv. citri).
1MAR-10-0s (pv. citri).
1MAR-10-92829;
1MAR-10-92829;
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01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 29.29
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 RDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERGINES CANNOTED TO SET AND S
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Xanthomonadaceae; Xanthomonas.
NCBL_TaxID=92829;
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SEQUENCE 769 AA; 83699 MW; B7995CA40A787593 CRC64;
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Pfam: PFO0627: response_reg; 1.
PRINTS; PRO0344; BCTRLSENSOR.
PRODOM: PRO0095; Response_reg; 1.
PROSITE; PS50109; HTS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
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77 VSTTKKLREMEVKSM - - IVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLM 134
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Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martine E.C., Meldanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., M., 194841 C.Y., Moon D.H., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.B., Teixaira B.C., Tezza R.I.D., Setubal J.C., Kitajima J.P.; Tanidade dos Santos M., Truindade dos Santos M., Truindade dos Santos M., Truindade dos Comparison of the genomes of two Xanthomonas pathogens with differing Nost specificities: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BB2000;
MEDLINE=99047557; PubMed-9829920;
MEDLINE=99047557; PubMed-9829920;
Belas R., Schneider R., Melch M.;
"Characterization of Proteus mirabilis precocious swarming mutants: identification of rsbA, encoding a regulator of swarming behavior.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.7%; Score 167.5; DB 16; Length 1364; 29.2%; Pred. No. 5e-06; ive 37; Mismatches 45; Indels 3;
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Last sequence update)
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Pfam; PF02518; HATPase_c: 1.
Pfam; PF02518; HATPase_c: 1.
Pfam; PF001627; HisKA; 1.
Pfam; PF001627; HisKA; 1.
Pfam; PF000785; PAC; 2.
Pfam; PF000785; PAC; 2.
Pfam; PF00078; PAC; 2.
PFNUTS; PR00034; BCTRLSENSOR.
PF000007; PF0000039; Response_reg; 2.
PROSTTE; PS5010039; CHASE; 1.
PROSTTE; PS50119; HTS_KIN; 1.
PROSTTE; PS50119; PAC; 2.
PROSTTE; PS50110; PAS; 2.
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MEDLINE=22022145; PubMed-12024217;

MAINTER A.C.R., Monteatro-Vitorallo C.B., Van Sluys M.A., Almeida N.F.,

A lives L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A camarotte G., Cannavan F., Cardooo J., Chambergo F., Ciaplna L.P.,

A constant R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

A Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

A Formighieri E.F., Franco M.C., Gargeio C.C., Gruber A., Lemos M.V.F.,

A Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A Moreira L.M., Novo M.T.M., Addeira A.M.B.N., Martinez-Rossis N.M.,

A Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira W.R.,

Spinola L.A.F., Takita M.A., Tandra R.B.,

A Trindade dos Santos M., Truffl D., Tsai S.M., White F.E.,

A Trindade dos Santos M., Truffl D., Tsai S.M., White F.E.,

Setubal J.C., Kitalina J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
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J. Bacteriol. 180:6126-6139(1998).
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 166.5; DB 2; Length 36.4%; Pred. No. 1.9e-06; Live 26; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1 SEQUENCE 507 AA; 57326 MW; F5DA2EAD9C35DEF5 CRC64;
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                                                                                                                                                                                                                                                                          Pfam; PF02518; HATPASS—C; 1.
Pfam; PF00512; HisRA: 1.
Pfam; PF00072; response_reg; 1.
Probom; PR00034; BCTRLSRNGR.
Probom; PD00039; Response_reg; 1.
SMART; SM00387; HATPASS—C; 1.
SMART; SM00388; HisRA: 1.
                                                                                                             HSSP; P06657; 2CHF.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR003561; His_kina.
InterPro; IPR005467; His_kinase.
InterPro; IPR001789; Response_reg.
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EMBL; AE012344; AAM41638.1; -.
                                                                               EMBL; AF071215; AAC82662.1; -.
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                                                              KINASES
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Q8P883
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18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1364 AA; 150167 MW; 48F1C5FBD9710316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.1%; Score 163.5; DB 16; 30.3%; Pred. No. 1.1e-05; ive 36; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50112; PAS; 2.
PROSITE; PS50110; RESPONSE_REGULATORY; 2.
COMPLE Proteome.
SEQUENCE 1364 AA; 150167 MW; 48FIC5FBI
                                 InterPro; IPR006189; CHASE.
InterPro; IPR003661; His_KinA.
InterPro; IPR003661; His_KinA.
InterPro; IPR003570; Hpt.
InterPro; IPR001570; PAC.
InterPro; IPR000100; PAC.
InterPro; IPR0000100; PAC.
InterPro; IPR00001001; PAC.
InterPro; IPR000014; PAC.
InterPro; IPR001789; Response_reg.
Pfam; PF00318; HATPase_c; I.
Pfam; PF00318; HATPase_c; I.
IPR003594; ATPbind_ATPase.
                       ct_sens_pr_C
                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO0229; sensory_box; PROSITE; PS50839; CHASE; 1. PROSITE; PS50109; HIS_KIN; 1. PROSITE; PS50113; PAC; 2.
                                                                                                                                                                                                                                                                                                                                                 pfam; PF00072; response_reg; 2. PRINTS; PR0044; BCTRLSENSOR. Pr000m; PD000039; Response_reg; IIGREPAMS; IIGR00229; sensory_box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.39
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                           PF00785; PAC; 2.
PF00989; PAS; 2.
                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                          Pfam;
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A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica response regulator protein DZ2.
                                                                                                                                                                                                                                                                                                                                                                                                           ABB92150
AAB96490
AAG21090
AAG21088
AAB25159
                                                                                                                                                                                                                       AAB73276
                                                                                                                                                                                                                                                                                                                                                                                AAY28483
ABG70784
                                                                                                                                                                                                                                                                                                                        AAW86007
AAY28484
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG28668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW81600
                                                          ABG70785
                                                                                                                                                                                                                                                       ABP73292
                                                                                                                                                                                                                                                                   AAB73274
                                                                                                                                                                                                                                                                                                                                                                  AAY28481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY42637 standard; Protein; 136 AA
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                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                8887
9900
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9322
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9222
11288
11298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wyatt P, Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-580449/49.
N-PSDB; AAZ22974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal transduction shatter resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica napus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09949046-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2000
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   AAY42637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
AAY42637
   Arabidopsis thalia
Arabidopsis thalia
A. thaliana D22AT3
Brassica response
Arabidopsis, thalia
Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica response
Brassica response
                                                                                                   August 13, 2003, 19:06:41; Search time 41 Seconds (without alignments) 526.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_19Jun03:*

| SIDS1/gcgdata/geneseq/geneseep-emb1/Aal980.DAT:*
| SIDS1/gcgdata/geneseq/geneseep-emb1/Aal981.DAT:*
| SIDS1/gcgdata/geneseq/geneseep-emb1/Aal982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal985.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal985.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal985.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal985.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal989.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/Aal990.DAT:*
                                                                                                                                                                                     1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY42653
AAG10549
AAG44439
AAY42645
AAY42652
AAG10550
AAG44440
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                                                                         - protein search, using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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678
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142
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Match
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79.4
76.0
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64.5
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osl histidine kina osl histidine kina osl pro osl paridone kina yeast SiN1 receive Herbicidally activ Putative P. usast human diagno

Candida albicans S cos-1 histidine ki Candida albicans C Human kinase-like

Eucalyptus grandis Histidine kinase C

Minimum DB seq Maximum DB seq

Database

4100000

Result No.

Title: Perfect score:

sequence:

OM protein

Run on:

Scoring table:

Searched:

Pseudomonas aerugi Histdine protein k Histdine protein k

E. coli Rscc recei Pseudomonas aerugi Pseudomonas aerugi

Brassica napus DZ2 Pinus radiata cell

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Matches
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                                                        The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for requiating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter delayed plants such as oilseed tape (Brassica napus). The present sequence represents a B. napus response regulator protein D22.
                                                                                                                                                                                                                                                                                                                                                                The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for requiating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present
                                                                                                                                                                                                                                                                                                                                               61 SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP 120
                                                                                                                                                                                                                                                                                 1 MATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60
                                                                                                                                                                                                                                                                                                    A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal transduction protein; dehiscence; male sterile plant; DZ2 gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica response regulator protein DZ2 putative peptide seguence.
                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                   100.0%; Score 678; DB 20; Length 135; 100.0%; Pred. No. 1e-67; ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY42653 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whitelaw C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 6; 71pp; English.
                           Claim 4; Fig 1; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             121 LTKDKIIPLINQLMDA 136
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                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-580449/49.
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                      136 AA;
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                                                                                                                                                                                       Sequence
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                                                                                                                                                         1 MATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
                                                                                                    Gaps
                                                                                                  0
sequence represents the B. napus DZ2 putative peptide sequence
                                                                  Length 136;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 8916.
                                                              100.0%; Score 678; DB 20;
100.0%; Pred. No. 1e-67;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 AAG10549 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                               121 LTKDKIIPLINQLMDA 136
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99US-0123180.
99US-0123548.
99US-0125788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2000 (first entry)
                                                                                 13 Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                  136 AA;
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04-MAY-1999;
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30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2000
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                                  Sequence
                                                                                                                                                                                                                                          61
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                                                                  Query Match
Best Local S
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18-0135353 18-0135629 18-0136622 18-0136829 18-0137829 18-0137724 18-0137502 18-0137502 18-0137502 18-013899 18-0138919 18-0138919 18-0139452 18-0139452	990S-0139455. 990S-0139456. 990S-0139456. 990S-0139458. 990S-0139459. 990S-0139460. 990S-0139461. 990S-0139461. 990S-0139462. 990S-0139462. 990S-013963. 990S-0140823. 990S-0140823. 990S-0140823. 990S-0140823. 990S-0140823. 990S-0140823. 990S-0140823. 990S-0140823. 990S-0140823. 990S-0141842. 990S-014280. 990S-014280. 990S-014280. 990S-014280.	10.5-0.14408: 10.5-0.14408: 10.5-0.14433: 10.5-0.14433: 10.5-0.14433: 10.5-0.14433: 10.5-0.14433: 10.5-0.14438: 10.5-0.14438: 10.5-0.14438: 10.5-0.14488: 10.5-0.14508: 10
MAY - 1999; JUN -	18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 22-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 24-JUN-1999; 25-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 27-JUN-1999; 28	- 70L-1999; - 70L-
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PR 02-Aug-1999; 99US-014638B.
PR 04-Aug-1999; 99US-0147204
PR 04-Aug-1999; 99US-0147204
PR 04-Aug-1999; 99US-0147204
PR 05-Aug-1999; 99US-0147302.
PR 05-Aug-1999; 99US-0147302.
PR 05-Aug-1999; 99US-0147303.
PR 10-Aug-1999; 99US-0147311.
PR 11-Aug-1999; 99US-0147311.
PR 11-Aug-1999; 99US-014933.
PR 12-Aug-1999; 99US-014933.
PR 12-Aug-1999; 99US-0149329.
PR 12-Aug-1999; 99US-0149329.
PR 20-Aug-1999; 99US-0151065.
PR 20-Aug-1999; 99US-0151065.
PR 20-Aug-1999; 99US-0151065.
PR 20-Aug-1999; 99US-0151080.
PR 20-CCT-1999; 99US-01508294.
PR 20-CCT-1999; 99US-01508294.
PR 13-CCT-1999; 99US-01508294.
PR 20-CCT-1999; 99US-01508294.
PR 20-CC

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20 - MAY - 1999;
24 - MAY - 1999;
25 - MAY - 1999;
26 - MAY - 1999;
27 - MAY - 1999;
28 - MAY - 1999;
20 - JUN - 1999;
20 - J
                                                                                                                                                                                                                                                                  55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
                                                                                                                                                                                                                                                                                             1 MATKSMGDIEK ----IKKKL-NVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVII 54
                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                   Gaps
                                                                                                                                                6;
                                                                                                   Query Match 79.4%; Score 538; DB 21; Length 142; Best Local Similarity 78.9%; Pred. No. 4.7e-52; Matches 112; Conservative 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 55668.
                                                                                                                                                                                                                                                                                                                                                   115 HCLAKPLTKDKIIPLINQLMDA 136
||| || || || || || || 11
|121 HCLEKPLTKAKIFPLISHLFDA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG44439 standard; Protein; 142 AA.
  99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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990S-0126785.
990S-0127462.
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990S-0128714.
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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04-MAY-1999;
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06-MAY-1999;
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19-MAY-1999;
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PR 02-AUC-1999; 99US-0146386.

PR 03-AUG-1999; 99US-0146388.

PR 03-AUG-1999; 99US-0146388.

PR 04-AUG-1999; 99US-0147202.

PR 04-AUG-1999; 99US-0147202.

PR 04-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147302.

PR 10-AUG-1999; 99US-0147303.

PR 10-AUG-1999; 99US-0147303.

PR 11-AUG-1999; 99US-0147303.

PR 11-AUG-1999; 99US-0144313.

PR 11-AUG-1999; 99US-0148341.

PR 12-AUG-1999; 99US-0148341.

PR 12-AUG-1999; 99US-0148341.

PR 20-AUG-1999; 99US-0148341.

PR 20-AUG-1999; 99US-014836.

PR 20-AUG-1999; 99US-014926.

PR 20-AUG-1999; 99US-014936.

PR 20-AUG-1999; 99US-0115936.

PR 20-AUG-1999; 99US-0115939.

PR 20-AUG-1
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents a D22 A. thaliana homologue D22AT3 putative peptide sequence.
                                                                                                                                                                                55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
                                                                                                                                                                                              61 HRDGEASFDLILMDKEMPERDGVSTTKKLREMKVTSMIVGVTSVADGEEERKAFMEAGLN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                              1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII
                                                                                                                                             Gaps
                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal transduction protein; dehiscence; male sterile plant; shatter resistance; oilseed rape; DZ2AT3 gene.
                                                                           Length 142;
                                                                                                       16; Indels
                                                                           Score 538; DB 21;
Pred. No. 4.7e-52;
8; Mismatches 16;
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Misc-difference 57
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                                                                                                                                                                                                                                        HCLAKPLTKDKIIPLINQLMDA 136
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                                                                                                                                                                                                                                                                                                                                   AAY42645 standard; Protein; 142
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99US-0161361.
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99US-0161992.
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Best Local Similarity 78.9%;
Matches 112; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
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N-PSDB; AAZ22978.
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28-OCT-1999;
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28-OCT-1999;
29-OCT-1999;
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21 VDDDPLNLIIHEXIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGVSTT 80
                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                    81 KKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 8917.
                                                                                                                                       AAG10550 standard; Protein; 104 AA
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05-MAR-1999;
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                                                                                                                                        55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVISLADNEEERRAFMEAGLN 114
                                                                             1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII 54
                                                                                            A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                 Signal transduction protein; dehiscence; male sterile plant; D22B gene; shatter resistance; oilseed rape; response regulator protein.
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                                                         6; Gaps
                                                                                                                                                                                                                                                                                                                            Brassica response regulator protein DZ2B putative peptide sequence.
                               76.0%; Score 515; DB 20; Length 142; 76.1%; Pred. No. 1.7e-49; ive 8; Mismatches 20; Indels 6
                                                                                                                                                                                     121 HCLEKPLTKAKIFPLISHLFDA 142
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                                                                                                                                                                                                                                                       AAY42652 standard; Protein; 116 AA.
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                                           Best Local Similarity 76.1
Matches 108; Conservative
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          Sequence 142 AA;
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34 IIKAIGGISQTANNGEBAVIIHRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIV 93

Query Match 64.5%; Score 437; DB 21; Length 104; Best Local Similarity 84.5%; Pred. No. 5.9e-41; Matches 87; Conservative 6; Mismatches 10; Indels 0; Gaps

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11-AUG-1999;
12-AUG-1999;
                                                                                                                           18-JUN-1999
                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
2 IIKTIGGISQTAKNGEEAVILHRDGEASFDLILMDKEMPERDGVSTTKKLREMKVTSMIV 61
                 94 GVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLMDA 136
                            Arabidopsis thaliana protein fragment SEQ ID NO: 55669.
                                                                                  AAG44440 standard; Protein; 104 AA.
                                                                                                                                                                                                                                                                                                             990S - 0126264
990S - 0126785
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                                                                                                                        18-OCT-2000 (first entry)
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14-MAY-1999;
14-MAY-1999;
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18-MAY-1999;
19-MAY-1999;
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21-MAY-1999;
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                                                                                                     AAG44440;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
62 GYTSVADQEEERKAFMEAGLNHCLEKPLTKAKIFPLISHLFDA 104
                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 23518.
                                                                                     AAG21089 standard; Protein; 70 AA
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24-MAY-1999;
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9905-0145216

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                   17-OCT-2000 (first entry)
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131 NQLMDA 136 SHLFDA 66

61

RESULT 11 AAG21088

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99US-0148171
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12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
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02-AUG-1999
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06 - JUL - 1999)
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28-JUL-1999;
02-AUG-1999;
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Gaps . 9 Length 71; Indels 31.4%; Score 213; DB 21; 73.4%; Pred. No. 3.7e-16; ive 3; Mismatches 8; AAB25159 standard; Protein; 261 AA. 9905-0149930 9905-015566 9905-0151066 9905-0151066 9905-0151066 9905-0151080 9905-0151930 9905-0151930 9905-0151930 9905-0151930 9905-0154039 9905-0154039 9905-0154039 9905-0154039 9905-0154039 9905-0154039 9905-0159295 9905-0159295 9905-0159295 9905-0159295 9905-0159295 9905-0159295 9905-0159295 9905-016094 9905-016094 9905-016096 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 9905-016098 Conservative Query Match Best Local Similarity Matches 47; Conserv 64 55 HRDG 61 HRDG 23-Aug-1999; 25-Aug-1999; 27-Aug-1999; 27-Aug-1999; 30-Aug-1999; 30-Aug-1999; 30-Aug-1999; 10-SEP-1999; 10-SEP-1999; 116-SEP-1999; 116-SEP-1999; 116-SEP-1999; 116-SEP-1999; 116-SEP-1999; 117-CCT-1999; 113-CCT-1999; 113-CCT-1999; 113-CCT-1999; 113-CCT-1999; 113-CCT-1999; 113-CCT-1999; 113-CCT-1999; 114-CCT-1999; 115-CCT-1999; 115-CCT-1999; 116-CCT-1999; 117-CCT-1999; 118-CCT-1999; 118-CCT-1999; 119-CCT-1999; RESULT 12
AAB25159
ID AAB25
XX
AC AAB25 

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AAB25159;

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AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
pine (Pinus radiata also known as Monterey pine). The protein sequences
are involved in cell signalling. The polynucleotide and protein
sequences can be used to modify the response of plant cells to external
signals e.g. environmental changes or pathogens during the growth and
development of a plant. They can be used to modify cell proliferation,
differentiation, elongation and survival, resistance to disease and
nutrient metabolism Examples of modifications which can be produced are
altered fruit ripening and senescence of leaves and flowers e.g. to
delay senescence and prolong the life of cut flowers or enhance
accepted of reproductive organs to engineer sterile plants. Other
modifications can be used to delay senescence in selected cell types or
organs providing fruit and vegetables which have a longer shelf life
between harvest and consumption, or to decrease branching frequency in
forest tree species giving long stretches of valuable knot-free clear
coverages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                              Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.8%; Score 202; DB 21; Length 261; 36.5%; Pred. No. 3.7e-14;
                                                Pinus radiata cell signalling involved protein SEQ ID NO:127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 36.5%; Fred. No. 3.7e-
Matches 42; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             claim 3; Page 104-105; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42644 standard; Protein; 67
                                                                                                                                                                                                                                                                                                                                                                                                                           Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                          11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                                99US-0228986
99US-0162866
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              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to external signals -
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                                                                                                                                                                                  Pinus radiata
                                                                                                                                                                                                                                                                                                                                  12-JAN-1999;
01-NOV-1999;
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an arther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents the partial fragment of B. napus D22B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RscC; antagonist; agonist; cytokinin receptor; receptor; signal transduction; histidine kinase; hormone; cell division; cell differentiation; agriculture; growth regulator; harvest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAT--KSMGDIEK----IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                Signal transduction protein; dehiscence; male sterile plant; D22B gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.4%; Score 192.5; DB 20; Length 67; Best Local Similarity 65.7%; Pred. No. 6.7e-14; Matches 44; Conservative 6; Mismatches 10; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli RscC receiver region of histidine kinase.
      Brassica napus DZ2B partial fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG70785 standard; Protein; 118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 5; 71pp; English.
                                                                                                                                                                                                                                                            Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2002; 2002EP-0005749.
                                                                                                                                                                       99WO-GB00905.
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                                                                                                                                                                                                                             (BIOG-) BIOGEMMA UK LTD.
                                                                                                                                                                                                                                                          Wyatt P, Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 IHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHRDGNA 67
                                                                                                                                                                                                                                                                                          WPI; 1999-580449/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                        N-PSDB; AA222975
                                                                                    Brassica napus
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                                                                                                               WO9949046-A1
                                                                                                                                                                       22-MAR-1999;
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                                                                                                                                           30-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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The invention discloses a method for analysing antagonist or agonist activity to a cytokinin receptor. The method comprises bringing a candidate substance into contact with a transformed cell, in which a necoding the receptor has been introduced, and then measuring the existence, or the quantity, of the intracellular signal transduction from the receptor expressed in the cell. The cytokinin receptor comprises an extracellular region of the receptor, transmembrane regions, a histidine kinase region and a receiver region of the kinase. The transmembrane receptor regions and kinase region of the mospeneous to each other and the receptor region is heterogeneous to them. Cytokinins are plant hormones relevant to cell division and differentiation of higher plants. The method is used for analysing agonist or antagonist activity to a cytokine receptor. A substance with agonist or antagonist activity to the receptor can be used in agriculture, as a plant growth regulator, e.g. after harvest. The advantage is that the candidate substances do not need to be prepared in such large amounts as in previous methods and that the method avoids the immensely long time to observe and evaluate the growth of the plant candidate substances of the plant steened is the E. coli receiver region of histidine kinase which can transmit signals to the cytokinin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial, PvrR, variant Pseudomonas, microorganism, gram negative,
phenotype-mediated antibiotic-resistance, gram-positive;
                                                                                                                                                                                                                                                                                                                                                                                                Analyzing agonist or antagonist activity of a substance for use as a plant growth regulator, comprises measuring intracellular signal transduction from a cytokinin receptor expressed in a cell contacted with the test substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 42; 47pp; English.
                                                                                                                                                                            (SUMO ) SUMITOMO CHEM CO LID.
                        15-MAR-2001; 2001JP-0073812.
29-JUN-2001; 2001JP-0198639.
29-JUN-2001; 2001JP-0198640.
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                                                                                                                                                                                                                                                Higuchi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                WPI; 2002-693041/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AA;
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                                                                                                                                                                                                                                                    Kakimoto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA026983;
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AAC AAO26
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16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated polypeptide comprising a PvrR (variant Pseudomonas) amino acid sequence having at least 50 % identity to a 399 residue amino acid sequence, given in the specification, where expression of the polypeptide, in a microorganism, affects phenotypemediated antibiotic resistance in the microorganism. The methods and compositions of the present invention are useful for the diagnosis, prevention and treatment of gram negative or gram-positive bacterial infection. This sequence represents a Pseudomonas protein used in the exemplification of the invention.
                                                                                                                                                                                                              New isolated PurR polypeptide and polynucleotide that regulates bacterial biofilm formation, useful for the diagnosis, prevention and treatment of gram-negative or gram-positive bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GVSTTKKLREMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.1%; Score 156.5; DB 2435.8%; Pred. No. 9.9e-09; tive 22; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: August 13, 2003, 19:11:13
he : 43 secs
                                                                                                                                                                                                                                                                                    Disclosure; Fig 5E; 185pp; English
                                            06-JUL-2001; 2001US-303286P.
16-APR-2002; 2002US-373233P.
           05-JUL-2002; 2002WO-US23242
                                                                                               (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                 ij
                                                                                                                                 Drenkard
                                                                                                                                                                    WPI; 2003-221608/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 AA;
                                                                                                                                                                                    N-PSDB; AAL55304
                                                                                                                                 Ausubel FM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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g
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Sequence 127, App Sequence 31348, A Sequence 29359, A Sequence 20395, A Sequence 17557, Appl Sequence 17557, Appl Sequence 24, Appl Sequence 220, Appl Sequence 220, Appl Sequence 25112, A Sequence 2514, Appl Sequence 2514, Appl Sequence 5134, Appl Sequence 5134,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
                                                                                                            August 13, 2003, 19:10:32; Search time 17 Seconds (without alignments) 338.487 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                      136 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-112-450-4
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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678
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Match Length DB
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Perfect score:
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No.
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-	Sequence 22216, A Sequence 31677, A	Sequence 6809, Ap	114, A	29564	18891				5430,	Sequence 117, App		-	5040,	Sequence 221, App	
US-09-328-352-6073 US-09-252-991A-22932	US-09-252-991A-22216 US-09-252-991A-31677	US-09-328-352-6809	US-09-252-991A-23/65 US-09-228-986-114	US-09-252-991A-29564	US-09-252-991A-16981	US-09-252-991A-17904	US-09-107-532A-6859	US-09-107-532A-6746	US-09-328-352-5430	US-09-228-986-117	US-09-134-001C-3779	US-09-328-352-7397	US-09-107-532A-5040	US-09-634-238-221	
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311	811	320	331 762	302	129	629	212	234	256	599	245	257	246	250	
18.1	17.8	17.3	17.0	16.7	16.6	16.6	16.4	16.4	16.3	16.2	16.1	16.1	16.0	16.0	
122.5	120.5		115.5	113	112.5	112.5	111.5	111.5	110.5	110	109	109	108.5	108.5	
7 7 8 7 8	0.0	32	333	35	36	3.7	- 00 - M	6	4	41	4.2	4	44	4.5	

## ALIGNMENTS

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RESULT 2
US-09-328-352-7973
US-09-328-352-7973
US-09-328-352-7973
US-09-328-352-7973
US-09-328-352-7973
US-09-328-352-7973
US-09-328-352
     Sequence 127, Application US/09228986

Patent No. 639918

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy
APPLICANT: Or INVENTION: and Their Use in the Modification of Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 127

LENGTH: 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 8%; Score 202; DB 4; Length 26 36.5%; Pred. No. 7e-16; tive 34; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Acinetobacter baumannii
US-09-328-352-7973
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US-09-228-986-127
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20395
LENGTH: 1627
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                                                                                                                                                                                                                                                                                                                      77 VSTIKKLREMEVKSMI--VGVTSLADN--EEERRAFMEAGLNHCLAKPLIKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                                                     | 1429 MSGSDLARSIRQEEFENGEEFEVVIIGLTADAQPEEIERC-IQAGMNECLIKPIGLD 1483
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Patent No. 593936
GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Apan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.7%; Score 147; DB 4;
31.9%; Pred. No. 3.3e-08;
tive 26; Mismatches 45
                                                                                                                                21.8%; Score 148; DB 4;
28.8%; Pred. No. 1.1e-08;
tive 33; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-09-252-991A-20395
Sequence 20395, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                           TYPE: PRT (CRGANISM: Pseudomonas aeruginosa US-09-252-991A-29359
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Matches 37; Conservative
                                                                                                                                                               Best Local Similarity 28.8 Matches 34; Conservative
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ADDRESSEE: Medlen &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
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US-08-843-530B-36
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SEQ ID NO 29359
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APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEEC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/094,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3138, Application US/09252991A

Sequence 3138, Application US/09252991A

Patent NO. 6551795

GUNERAL INFORMATION:

APPLICANT: MAIC J. Rubenfield et al.

APPLICANT: MAIC J. RUBERC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR PLILING DATE: 1998-02-18

PRIOR PLILING DATE: 1998-07-27

NUMBER OF SEQ ID NO 31338

SEQ ID NO 31338

LENGTH 1010
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                                                                                                                                                                                                                                                 72 PERDGVSTTKKLREM-----EVKSMIVGVT--SLADNEEERRAFMEAGLNHCLAKPLTK 123
                                                                                                                        16 ENVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSS----FDLILMDKEM 71
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22.1%; Score 150; DB 4; Length 1014;
Best Local Similarity 25.5%; Pred. No. 7.4e-09;
Matches 35; Conservative 36; Mismatches 56; Indels 19
                         Length 946;
                         Query Match 22.5%; Score 152.5; DB 4; Length Best Local Similarity 30.2%; Pred. No. 3.4e-09; Matches 39; Conservative 34; Mismatches 41; Indels
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US-09-252-991A-31338
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61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFMEAGLNH 115
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                                                    95 EATRLIRREERAQGWPRVPIVALTAHILD--EHRRAGIEAGMDAYLGKPVDRAELYATLE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osmosensing Histidine Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.6%; Score 139.5; DB 2; Best Local Similarity 31.1%; Pred. No. 1.8e-07; Matches 42; Conservative 28; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Apnan, Jascqueline
APPLICANT: Alox, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histi
WUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38.230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPACK: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 220 Montgomery Street, Su
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08843530B Patent No. 593906 GENERAL INFORMATION: GENERAL SELITERDINKELY SELITERDINKELY Claude
                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08843530B
Patent No. 5939306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1188 YESKPLQONHLIQTI 1202
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LENGTH: 1281 amino acids
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                                                                                                                 132 QLM 134
                                                                                                                                                                153 RLL 155
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US-08-843-530B-2
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APPLICANT: MARC J. RUBEDIfield et al.

APPLICANT: MARC J. RUBEDIfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1080 DDDKNETSVKILVVEDNHVN----QEVIKRMLNLEGIENIELACDGQEAFDKVKELTSKG 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 SSFDLILMDKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 DIEKIKKKLNVLIVDDDPLNLIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTIN RAIPS:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
ATTORNEY APPLICATION: 435
ATTORNEY APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.4%; Score 145; DB 2; Best Local Similarity 29.0%; Pred. No. 3.8e-08; Matches 40; Conservative 40; Mismatches 44,
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET UNBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
INPORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-17557
; Sequence 17557, Application US/09252991A
; Patent No. 6551795
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US-09-252-991A-17557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1220 amino acids
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Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
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FILING DATE: 16-APR-1997
CIASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 220 Montgomery Street, Su.
TTY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/08843530B Patent No. 5939306
GENERAL INFORMATION:
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MDIUM TYPE: Floppy disk
CMEDUWTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1188 YLSKPLQQNHLIQTI 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Adnan, Jacqueline
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                            TITLE OF INVENTION: Osmosensing Histidine Kinases NUMBER OF SEQUENCES: 36
CORRESSOUNDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Monitoomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                     COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.6%; Score 139.5;
31.1%; Pred. No. 1.8e
tive 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MACKNIGHT, KAMTIN T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08843530B Patent No. 5939306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
  Agnan, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 CLAKPLTKDKIIPLI 130
                    Alex, Lisa A.
Simon, Melvin I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.1%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide US-08-843-530B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1298 amir
TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                COUNTRY: UN
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-843-530B-4
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61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFMEAGLNH 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: MacKnight, Kamin F.
REGISTRATION NUMBER: UTC-02717
TELECOMMUNICATION NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 795-8410
TELEPHONE: (415) 795-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Adax, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kina, NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
SIREET: 22 Montgomery Street, Suite 2200
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.118

FULLE REPERENCE: 107196.118

FULLE REPERENCE: 1099-02-18

PRIOR PAPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25928

LENGTH: 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADN--EEERRAFMEAGLNHCLAKPL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 KSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 STIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.4%; Score 138.5; DB 4; Length 234; Best Local Similarity 30.2%; Pred. No. 2e-08; Matches 35; Conservative 31; Mismatches 47; Indels 3
                         APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: O'Toole, Paul W.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them and methods for using them.
FILE REPERBNCE: 11000.104301
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: RESESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-252-991A-26112
; Sequence 26112, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25928, Application US/09252991A patent No. 6551795 Application ROWANTION APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Lactobacillus rhamnosus US-09-634-238-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25928
       Christensson, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            729 KRAEL 733
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-09-252-991A-25928
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LENGTH: 234
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APPLICANT: MARC J. RUBERIGLE AL.
APPLICANT: MARC J. RUBERIGLE AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: APPLICANT NUMBER: US/09/252, 991A
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 33142
LENGTH: 1441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                                                                                         2 ATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGS 60
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                                                                                                                                                                                                                                                                        Length 1298;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                        Query Match 20.6%; Score 139.5; DB 2; Best Local Similarity 31.1%; Pred. No. 1.8e-07; Matches 42; Conservative 28; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28143, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 220, Application US/09634238
Patent No. 6544772
GENERAL INFORMATION:
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Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
3-08-843-570-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||| :: :| |
1188 YLSKPLQQNHLIQTI 1202
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Best Local Similarity 28.8%
Matches 34; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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Patent No. 555195

SGREARL INFORMATION:
APPLICART: MARC J. RUBENfield et al.
APPLICART: MARC J. RUBENfield et al.
APPLICART: MARC J. RUBENFICATION:
TITLE OF INVENTION: NEGGGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
FILE REPERBUCE: 107196.136
CURRENT PELING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

CURRENT FILING DATE: 1998-02-18

SEQ ID NO 26112
LENGTH: 860

LENGTH: 860

COURTY MATCH: 860

TYPE: PRY

OCAMAISM: PREDICATION NUMBER: US 60/094,190

TYPE: PRY

OCAMAISM: PREDICATION NUMBER: US 60/094,190

AMATCHES 36; CONSETVATIONS NO. 38-07;
MATCHES 36; Indels 9; Gaps 3;
MARCHES 36; CONSETVATION NO. 35-07;
MATCHES 36; CONSETVATION NO. 36-07;
MATCHES 36; CONSETVATION NO. 3
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Search completed: August 13, 2003, 19:13:02 Job time : 18 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Sequence 127, App	Seguence 8, Appli	Sequence 328, App	Sequence 909, App		Sequence 366, App	Sequence 2, Appli	Sequence 7, Appli	Sequence 10049, A	Sequence 4, Appli	Sequence 17, Appl	Seguence 11131, A	Sequence 12532, A	Sequence 9975, Ap	Sequence 13783, A
SUMMAKIES	ď.		US-10-101-464A-127	US-09-918-508-8	US-09-801-368-328	US-10-101-464A-909	US-09-801-368-332	US-09-801-368-366	US-10-126-120-2	US-09-918-508-7	US-10-156-761-10049	US-09-424-951-4	US-10-135-322-17	US-09-815-242-11131	US-10-156-761-12532	US-10-156-761-9975	US-09-815-242-13783
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	% Query Match Tenath DB	nelly CII	261	118	622	1018	1220	712	974	125	1829	1081	2150	227	203	227	232
	& Query		29.8	25.3	22.1	21.5	21.4	21.2	20.3	20.2	19.5	18.9	18.8	18.7	18.6	18.5	18.4
	9	20016	202	171.5	150	146	145	143.5	137.5	137	132	128	127.5	126.5	126	125.5	124.5
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Sequence 2, Appli Sequence 4, Appli Sequence 54, Appl	8624 1260	956, 12098	e 1374	Sequence 11629, A Sequence 10420, A			• •					•	_	•	-		edneuce		ednence		ednence	ednence	Sequence 10458, A
US-10-116-0 US-10-116-0 US-09-769-7	5 US-10-156-761- 5 US-10-156-761-	5 US-10-101-4 US-09-815-24	5 US-10-156-7	US-09-815-24 US-09-815-24	5-10-101-4	US-10-135-3	0 US-09-918-508-2	5 US-10-156-761-1	5 US-10-101-464A-11	5 US-10-156-761	2 US-10-100-294A-27	5 US-10-156-761-100	0 US-09-738-626	1 US-09-819-14	0 US-09-918-5	4 US-10-135-32	1 US-09-819-142-10	5 US-10-101-464A-1	5 US-10-101-464A-	5 US-10-101-464A-9	4 US-10-135-322-2	4 US-10-135-322-18	5 US-10
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2471 181																							
188.3							17.3					16.5		16.4	- 1	_	- 2		16.2				
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16 17	110	21	23	22.4	26	2.0	00	30	31	32	93	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 US-10-101-464A-127 Publication No. GENERAL INFORMAT APPLICANT: STRA APPLICANT: Hig TITLE OF INVENT TITLE OF INVENT FILE REFERENCE: CURRENT APPLICATI FILE REFERENCE: CURRENT APPLICATI FILE REFERENCE: CURRENT APPLICATI FILE REFERENCE: CURRENT APPLICATI FRIOR FILING DA PRIOR FILI	plication US/101 US20030046728A1 ION: Ubelling William Wilco Bala, Timothy Ubelling Composition Gins, Colleen M. ION: Composition ION: Composition ION: and Their 11000.1020c2 TION: NUMBER: 09/70 ON NUMBER: 09/70 ON NUMBER: 09/70 ON NUMBER: 09/70 TE: 1999-01-12 TE: 1999-01-12 TE: 1999-01-12 TE: 1999-01-12 TE: 1999-01-12 E: 1999-01-12 E: 1999-01-13 ION NUMBER: PCT/U ON NUMBER: PCT/U
Best Loc Matches	al Similarity 42; Conserva
Qy Db	18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77 :
δy	78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQ 132

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US-09-801-368-332
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REPERENCE: 109272.147
CURRENT PILING DATE: 2001-03-07
CURRENT FILING DATE: 2001-03-07
PRIOR PILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 4440
SOFTWARE: PATENTIN VEXSION 3.0
SEQ ID NO 328
LENGTH: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 63
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KATHOTO, TATSUO
APPLICANT: HIGUCHI, MASAYUKI
APPLICANT: HIGUCHI, MASAYUKI
APPLICANT: HIGUCHI, MASAYUKI
APPLICANT: HOUGE, TSUTOMO
TITLE OF INVENTION: TO CYTOKININ RECEPTOR
FILE REFERENCE: 065478
CURRENT APPLICATION NUMBER: US/09/918,508
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 25.3%; Score 171.5; DB 10; Length 118; Best Local Similarity 33.9%; Pred. No. 3.2e-11; Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps
78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 RLIQRIRQLGLILEVIGVTANALAEEKQRC-LESGMDSCLSKPVILDVI 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 328, Application US/09801368 ; Patent No. US20020128250A1
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                                                                                                         US-09-918-508-8; Sequence 8, Application US/09918508; Patent No. US20020177162A1
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Escherichia coli
US-09-918-508-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Busby, Robert
Cali, Brian
APPLICANT: Cali, Petan
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
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Milne, Todd
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APPLICANT:
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Miewenhuizen, Nicolaas
APPLICANT: Miewenhuizen, Nicolaas
APPLICANT: Miewenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000/1020-203-18
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2000-11-01
PRIOR FILING DATE: 1000-203-18
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: E0/162,866
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR PELING DATE: 1999-01-11-01
PRIOR PELING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                        373 LRKGFHVLLVEDDAVSIQLCSKFLRKYGCTVQVVSDGLSAISTLEKYR----YDLVLMD 427
                                                                                                                                                                                                                                                   69 KEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI-- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     916 DLILMDVCMPVMNGLQATRIIRSFEEMGNWDAAVNAGIELVSSDLSCNGHSSRESKERVP 975
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                                                                                                                            12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.5%; Score 146; DB 15; Length 1018;
25.2%; Pred. No. 4e-07;
tive 35; Mismatches 53; Indels 34; Gaps
                                                                   20;
Length 622;
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Ouery Match 22.1%; Score 150; DB 10;
Best Local Similarity 28.1%; Pred. No. 7.3e-08;
Matches 38; Conservative 32; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 909, Application US/10101464A publication No. US20030046728A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 332, Application US/09801368; Patent No. US20020128250A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   127 ----- 1PLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                            487 ILIRYLKDRIPLCEQ 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.28
Matches 41, Conservative
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-101-464A-909
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Sequence 2. Application US/10126120
Sequence 2. Application US/10126120
EDBEAL INFORMATION:
APPLICANT: SARAKAbara, Hitcshi
APPLICANT: SARAKAbara, Hitcshi
APPLICANT: Takei, Kentaro
TITLE OF INVENTION: MCROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FAC
FILE REFERENCE: 11127-004001
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US/10/126,120
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5: 50
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                                                                                                                                                                                                                                                                              17 NVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVII----HRDGGSSFDLILMDKEMP 72
                                                                                                                                                                                                                                                                                                                                                                       -----MIVGVISLADN 101
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Patent No. US20020177162A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: RAINOTO, TATSUO
APPLICAMT: HIGUGH, MASAVUKI
APPLICAMT: INOUE, TSUTOMU
APPLICAMT: INOUE, TSUTOMU
TITLE OF INVENTION: AT CYTOKININ RECEPTOR
FILE REFERENCE: G65478
CURRENT APPLICATION NUMBER: US/09/918,508
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-03-15
                                                                                                                                                               31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.3%; Score 137.5; DB 15; Length 974; 24.6%; Pred. No. 3.2e-06; ...tive 32; Mismatches 46; Indels. 29;
                                                                                     Query Match
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 ERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRA---
                                                                                                                                                                                                                                                                                                                                                                          70 EMPERDGVSTTKKLREMEVKS------
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616 MDKRKALL-SGCNDYLTKPV 634
; ORGANISM: Saccharomyces cerevisiae US-09-801-368-366
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Best Local Similarity 24.6%
Matches 35; Conservative
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US-09-918-508-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.4%; Score 145; DB 10; Length 1220; Best Local Similarity 29.0%; Pred. No. 6.6e-07; Matches 40; Conservative 40; Mismatches 44; Indels 14
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Milne, Todd
No. US20020128250Alman, Thea
                                                                                        Milne, Todd
No. US20020128250Alman, Thea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 366, Application US/09801368; Patent No. US20020128250A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332
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SOFTWARE: Patentin version 3.0
SEQ ID NO 366
LENGTH: 712
TYPE: PRT
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Sherman, Amir
Silva, Jeff
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APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Revin
                                                                                                                                                                                            Salama, Sofie
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                                                       Maxon, Mary
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US-09-801-368-366
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US-10-135-322-17
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                                                                                                                                                                                                                                                                                                                                           Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                              37; Indels
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Best Local Similarity 31.5%; Score 132; DB 15;
Best Local Similarity 31.5%; Pred. No. 3.1e-05;
Matches 39; Conservative 24; Mismatches 51;
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| Publication No. US20030119018A1
| Publication No. US20030119018A1
| APPLICANT: OVURA, SATOSHI
| APPLICANT: SHIRAMA, HARUO
| APPLICANT: SHIRAMA, HIROSHI
| APPLICANT: SHIRAMA, HIROSHI
| APPLICANT: SHIRAMA, HONGHI
| APPLICANT: SAKAKI, YOSHIVKI
| APPLICANT: SAKAKI, YOSHIVKI
| APPLICANT: APATORI, MASAHIRA
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| FILE REFERENCE: 249-262
| CURRENT FILING DATE: 2001-05-39
| PRIOR FILING DATE: 2001-05-39
| PRIOR FILING DATE: 2001-05-30
| PRIOR FILING DATE: 2001-08-02
| PRIOR FILING DATE: 2001-08-02
| NUMBER: OF SEO ID NOS: 15109
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; Patent No. US20020137034A1
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2
SEQ ID NO 7
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LENGTH: 1829
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                                                                                                                       LENGTH: 125
                                                                                                                                                                          TYPE: PRT
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2024 RKK--ALIVEDNELNRKVLAQLFKKIDWTISFAENGREA-LKEITGERCFDIVFMDCQMP 2080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LILMDKEMPERDGVSTTKKLREMEVKS------MIVGVTS---LADNEEERRAFME 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 KKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                APPLICANT: SOLL, DAVID R.

TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE,
TITLE OF INVENTION: CANINI, AND USE THEREOF
FILE REFERENCE: 087714/0118.
CURRENT APPLICATION NUMBER: US/09/424,951
CURRENT FILING DATE: 2000-01-20
PRIOR PELING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/048,914
PRIOR APPLICATION NUMBER: 60/048,914
PRIOR PELING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 ERDGVSTTK----KLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLT 122
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APPLICANT: HELRERIUTTA, Y
APPLICANT: HELRERIUTTA, Y
APPLICANT: HELRERIUTTA, Y
APPLICANT: MAHONEN, AP
APPLICANT: SAUPETINEN, L
APPLICANT: RAUPETINEN, L
APPLICATION NUMBER: US/10/135,322
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALENTIN Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.5%; Pred. No. 0.00012;
Matches 37; Conservative 20; Mismatches 50; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.9%; Score 128; DB 10; Length 10 Best Local Similarity 28.3%; Pred. No. 4e-05; Matches 43; Conservative 31; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:::::||| : ::||| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/10135322 Publication No. US20020173017A1 GENERAL INFORMATION:
APPLICANT: SRIKANTHA, THYAGARAJAN APPLICANT: SOLL, DAVID R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Arabidopsis thaliana US-10-135-322-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Candida albicans US-09-424-951-4
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65 ILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 DGVSTTKKLREMEVKSMIVGVTSLAD--------NEEERRAFMEAGLNHCLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 EKIKKKLNVLIVDDDPLNLIIHEKIIKAIG---GIS--QTANNGEEAVIIHRDGGSSFDL 64
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                                                                                                                                                                                                                                                                                                                                                                                17 NVLIVDDDPLNLIIHEKIIKAIGGISQ--TANNGEEAVIIHRDGGSSFDLILMDKEMPER 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.5%; Score 125.5; DB 15; Length 227; Best Local Similarity 29.2%; Pred. No. 8.6e-06; Matches 38; Conservative 28; Mismatches 53; Indels 11; Gaps
                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                          Length 203;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                       Query Match
18.6%; Score 126; DB 15;
Best Local Similarity 29.5%; Pred. No. 6.5e-06;
Matches 36; Conservative 20; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squence 9975, Application US/10156761
Squence 9975, Application US/10156761
Squence Application No. US20030119018A1
GENERAL INPORMATION:
APPLICANT: OMORA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: HSHIKAWA, JUN
APPLICANT: HSHIKAWA, HROSHI
APPLICANT: HSHIKAWA, HROSHI
APPLICANT: HATTORI, MACHIRA
APPLICANT: HATTORI, MACHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PELICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SSD ID NO 9975
LENGTH: 227
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12532
LENGTH: 203
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US-09-815-242-13783
; Sequence 13783, Application US/09815242
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                                                                                                                                                         ; ORGANISM: Streptomyces avermitilis
US-10-156-761-12532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 227;
                                                                                                                                                                                                                                                                                    APPLICANT: Wall, Dannel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DADIE: 2001-03-21
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,846
PRIOR APPLICATION NUMBER: 60/206,846
PRIOR PLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/205,578
PRIOR PLICATION NUMBER: 60/205,578
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2001-12-27
PRIOR PLILING DATE: 2001-12-27
PRIOR PLILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 11-31
LENGTH: 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
18.7%; Score 126.5; DB 9;
Best Local Similarity 29.1%; Pred. No. 6.7e-06;
Matches 34; Conservative 30; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 12522, Application US/10156761
; Publication No. US20030119018A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OKUTA, SATOSHI
APPLICANT: ISHIRAWA, JUN
APPLICANT: HEBA, TARNON
APPLICANT: SHIRAWA, HEBOSHI
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: APADAYOSHI
APPLICANT: APADAYOSHI
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: APATORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-39
PRIOR FILING DATE: 2001-05-30
                                                                                                               Sequence 11131, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGANISM: Haemophilus influenzae US-09-815-242-11131
                                                                                                                                                                                                                      Ohlsen, Kari E.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-10-156-761-12532
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18.4%; Score 124.5; DB 9; Length 232; 28.2%; Pred. No. 1.1e-05; tive 31; Mismatches 48; Indels 5;
                                                                                                                            APPLICANT: Haselbeck, Kobert
APPLICANT: Obleson, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Transmoto. Robert T.
APPLICANT: Yanamoto. Robert T.
APPLICANT: Yanamoto. Robert T.
APPLICANT: Yanamoto. Robert T.
APPLICANT: Yanamoto. Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 2001.14
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-24
PRIOR PLILING DATE: 2000-05-24
PRIOR PLILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-10-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-10-22
PRIOR PLILING DATE: 2000-10-22
PRIOR FILING DATE: 2000-10-26
NUMBER OF EXQ ID NOS: 14110
SCPTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 13783
LENGTH: 232
LENGTH: 232
LENGTH: 232
LENGTH: 232
LENGTH: 232
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Matches 33; Conservative
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ORGANISM: Salmonella typhi
US-09-815-242-13783
Patent No. US20020061569A1
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78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLM 134 Óγ

:|:|||| : ::::: | | |::||:|: | | ||::||: | 4 ILLVDDDRELTSLLKELLEMEGENVLVAHDGEQALELLDD---SIDLLLLDVMMPKKNGI 60 18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77

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5; Gaps

Search completed: August 13, 2003, 19:20:55 Job time : 55 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 19:09:57; Search time 19 Seconds (without alignments) 688.365 Million cell updates/sec Run on:

Title:

US-09-646-679-15 678 1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136 Perfect score: Sedneuce:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	histidine kinase h	O)		ui.	sensor histidine k	sensor protein Rcs		+	hypothetical prote	two component sens		aerobic respiratio	response regulator	sensor histidine k.	two-component hybr	sensory box histid	chemotaxis protein	sensory box histid	response regulator	sensor histidine k	sensory box histid		ax1	sensor histidine k	sensory transducti	sensory transducti	aerobic respinátio	compone	cell wall assembly
SUMMARIES	QI	108875	G65010	o	œ	H87640	AD0790	BVECCC	191017	E85861	AD0149	E87644	043	948	215	39	387252	96	A87580	369422	$\sim$	A87617	ന	4	~	750	875525	60	AB0032	A49344
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RESULT 2

G65010

Sensor protein evgs (EC 2.7.3.-) precursor - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 01-Mar-2002

C;Accession: G65010; J00221; I41200

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M., A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

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A83324	KGECAK	A91140	D85985	E83529	F83153	S48387	E87460	C82424	E83212	S64828	C87575	D87559	AI0860	H97516	B41863
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22.1	77.7	22.1	22.1	21.8	21.7	21.4	21.3	21.2	21.2	21.2	21,1	21.0	21.0	20.9	20.9
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## ALIGNMENTS

RESULT 1 T08975 histidine kinase homolog DHKB - slime mold (Dictyostellum discoideum) N;Alternate names: hybrid histidine kinase DHKB C;Species: Dictyostellum discoideum C;Dacession: T08875 R;Zinda, M.J; Singleton, C.K. Dev. Biol. 1999 #sequence_revision 11-Jun-1999 #text_change 11-May-2000 C;Accession: T08875 R;Zinda, M.J; Singleton, C.K. Dev. Biol. 196, 171-183, 1983 A;Title: The hybrid histidine kinase dhkB regulates spore germination in Dictyostellu A;Reference number: Z16506; MUID:98248997; PMID:9576830 A;Accession: T08875 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Cross-references: EMBL,AF024654; NID:92460283; A;Cross-references: EMBL,AF024654; NID:92460283; A;Cross-references: EMBL,AF024634; NID:92460283; A;Gene: dhkB A;Introns: 790/3 C;Genefics: A;Gene: dhkB A;Introns: 790/3 C;Superfamily: response regulator homology <a href="https://cross-references/best-rans-membrane-protein">C;Keywords: protein kinase; transmembrane protein F;1841-1964/Domain: response regulator homology <a href="https://cross-references/best-rans-membrane-protein">C;Keywords: protein kinase; transmembrane-protein F;1841-1964/Domain: response regulator homology <a href="https://cross-references/best-rans-membrane-protein">C;Keywords: protein kinase; transmembrane-protein F;1841-1964/Domain: response regulator homology <a href="https://cross-references/best-rans-membrane-protein">C;Keywords: protein kinase; transmembrane-protein</a></a></a></a>	Query Match  26.7%; Score 181; DB 2; Length 1969;  Best Local Similarity 35.8%; Pred. No. 5.6e-07;  Matches 48; Conservative 29; Mismatches 39; Indels 18; Gaps 5;  QY
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Secretary histidine kinase/response regulator [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001
C;Accession: H87640
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
B.; Laub, M.T.; DeBoy, R.T., Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
D, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Feference number: A87249; MUID:21173698; PMID:111259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cobable sensor for regulator EvgA evgS [imported] - Escherichia coli (strain O157:H7 cobable sensor for regulator EvgA evgS [imported] - Escherichia coli (strain O157:H7 cobate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 cobate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 cobate: 16-Feb-2001 cobate: 17-Feb-2001 coba
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                                                        72 PERDGVSTIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLIN 131
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                                                                                                                                                                                                 72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
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                 12 IKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM
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C;Superfamily: evgS protein; response regulator homology
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25; Mismatches
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Best Local Similarity 34.4%
Matches 42; Conservative
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A.Accession: JU0221
A.Accession: JU0221
A.Accession: JU0221
A.Accession: JU0221
A.Accession: JU0221
A.Status inucleic acid sequence not shown
A.Residues: 1-151, F', 153-241, PL', 244-274, R', 276-419, FE', 422-738, D', 740-757, K', 759-8, Ftytsuml, R.; Katayama, S.; Taniguchi, M.; Horie, T.; Ikeda, M.; Igaki, S.; Nakagawa, H. Gene 140, 73-77, 1994
A.Title: Newly identified genes involved in the signal transduction of Escherichia coli A. Accession: 141200
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Molecule Type: DNA
A. Residues: 1-151, Fr. 153-241, PL', 244-274, R', 276-419, FE', 422-738, 'D', 740-757, K', 759-
A. Cross-references: GB:D14008; NID:9456162; PIDN:BAA03108.1; PID:9216554
C. Genetics:
C. Genetics:
C. Superfamily: evgS protein; response regulator homology
C. Reywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase; t. Fr. 87-935, Domain: sensor histidine kinase homology SAHK>
Fr. 87-1070, Domain: sensors regulator homology SAHK>
Fr. 81-1070, Domain: response regulator homology SAHK>
Fr. 81-1070, Pomain: response regulator homology RAHP>
Fr. 81-1009, Mainding site: phosphate (Als) (covalent) #status predicted
A; Accession: G65010
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1.1197 CBLAT>
A; Cross-references: GB: AE000325; GB: U00096; NID: 91788709; PIDN: AAC75429.1; PID: 91788713;
A; Experimental source: strain K-12, substrain MG1655
B; Utsumi, R:
Submitted to JIPID, January 1993
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C;Superfamily: evgS protein; response regulator homology
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llarity 34.4%; Pred. No. 5.1e-07;
Conservative 25; Mismatches 52;
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Matches 42; Conserv
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sensor for ctr capsule biosynthesis [imported] - Escherichia coli (strain O157:H7, su cispecies: Escherichia coli (cjatei 18-uul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: C91017; R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C;Accession: C91017; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and characteric complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and characteric control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
A;Title: RcsB and RcsC: a two-component regulator of capsule synthesis in Escherichis A;Reference number: JV0068; MUID:90130299; PMID:2404948
A;Accession: JV0069
A;Accession: JV0069
A;Rolecule type: DN
A;Residues: 1-112. DN
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A/Gene: rosc.
A/Gene: rosc.
C/Superfamily: rosc protein; response regulator homology
C/Superfamily: rosc protein; capsule synthesis; phosphohistidine; phosphoprotein,
C/Keywords: autophosphorylation; capsule synthesis; phosphohistidine; phosphoprotein,
C/Keywords: autophosphorane #status predicted <TMI>
C/Keywords: transmembrane #status predicted <TMI>
C/Keywords: autophosphorane #status predicted <TMI>
C/Keywords: autophosphorane #status predicted
C/Keywords: autophosphorane #status (Covalent) #status predicted
C/Keywords: phosphore (His) (covalent) #status predicted
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-933 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36530.1; PID:g13362576; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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Nilternate names: regulatory protein rcsC
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Ribattner, F. R.: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
Ribattner, F. R.: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Reference number: A64720; MuID:97426617; PMID:9278503
A; Recession: H64991
A; Residues: H64991
A; Residues: 1-933 CBLAT>
A; Cross-references: GB; RE00311; GB:U00096; NID:91788547; PIDN:AAC75278.1; PID:91788548;
A; Experimental source: strain K-12, substrain MG1655
A; Cross-references: strain K-12, substrain MG1655
B; Stout, V.; Gottesman, S.
J; Bacteriol. 172, 659-669, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretary protein RcsC (EC 2.7.3.-) [imported] - Salmonella enterica subsp. enterica serova C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C; Accession: AD0790 R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; MUID:21534947; PMID:11677608 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accession: AD0790 A; Accessi
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A;Residues: 1-948 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07502.1; PID:916503497; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                 262 RSAHILIVDDNATNRAVAEALCDMFECTSEQAVDGVEAVEMARSG--RFDLILMDIKMPR 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 RDGVSTTKKLREMEVKSMIVGVTSLADNEE--ERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
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                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: rcsC
C;Superfamily; rcsC protein; response regulator homology
C;Keywords: phosphotransferase
                                                                                                          49;
                                   ed. No. 3.4e-07;
Mismatches 49
                                                 Pred. No.
                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 33.9%
hes 37; Conservative
                                   Best Local Similarity 31.79
Matches 39; Conservative
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Gaps

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Indels

Length 933;

7

Gaps

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Gaps

Indels

Length 642;

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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Paccession: Ab06432
C;Paccession: Ab06432
R:Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: Ab0001; MUID:21470413; PMID:11586360
A,Gene: arcB
C,Superfamily: aerobic respiration control sensor protein arcB; response regulator ho
C,Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aerobic respiration control sensor/response regulatory protein (EC 2.7.3.-) [imported
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-642 <STO>
A.Cross-references: GB:AE005673; NID:913424865; PIDN:AAK25153.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 GVEATHRIRAFNSPAGAAPILAMTANAMAHQQASYLAAGMDGAIAKPLS
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24.0%; Score 162.5; DB 2;
Best Local Similarity 33.0%; Pred. No. 5.5e-06;
Matches 36; Conservative 28; Mismatches 40;
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Best Local Similarity 27.0%,
Matches 33; Conservative
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A; Status: preliminary
A; Molecule type: DNA
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A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Accession: EBS861
A; Accession: EBS861
A; Residues: Preliminary
A; Monte and A; Residues: 1-033 < CSTO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Versinia pestis
C; Species: Versinia pestis
C; Species: Versinia pestis
C; Species: Versinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C; Accession: AD0149
B; Parthill; J; Wateh
B; W; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A.; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-957 < KUR>
A; Residues: 1-957 < KUR>
A; Conetics:
C; Genetics:
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C;Superfamily: rcsC protein; response regulator homology
C;Keywords: phosphotransferase
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Best Local Similarity
Matches 37; Conserv
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response regulator homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Daccession: A69487
C;Accession: A69487
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.S.
Smith, H.O.; Woese, C.R.; Venter, J.S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Shith, H.O.; Mcose, C.R.; Venter, J.C.
Shith, H.O.; Mosse, C.R.; Venter, J.
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A; Residues: 1-736 <HED:
A; Cross-references: GB: AE004259; GB: AE003852; NID: 99656353; PIDN: AAF94979.1; GSPDB: GN001
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
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A;Areference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82151
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.5%; Score 159; DB 2; 28.3%; Pred. No. 1.5e-06; tive 42; Mismatches 31;
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Best Local Similarity 28.3%
Matches 36; Conservative
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A;Gene: VC1831
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C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #text_change 09-Dec-2002 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AG1897 B;Kaneko, T.; Makamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriqua Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                            PCC
                                                                                                                                                                                                                                                two-component hybrid sensor and regulator all0729 [imported] - Nostoc sp. (strain
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A;Status: preliminary
A;Modecule type: DNA
A;Modecule type: DNA
A;Residues: 1-1645 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72686.1; PID:g17130074; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a110729
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escherichia bacillus su caulobacter

escherichia alcaligenes xanthomonas

Q8x613 P10957 O34534 Q45284 Q46284 Q46084 Q46086 P51358 P51358 Q66065 Q78428

escherichia

thermotoga porphyra pu pseudomonas escherichia guillardia

ALIGNMENTS

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STRAIN-K12;
MEDLINE-93173621; PubMed-1289796;
MEDLINE-93173621; PubMed-1289796;
Utsuni R., Katayama S., Ikeda M., Igaki S., Nakagawa H., Miwa A.,
Taniguchi M., Noda M.;
"Cloning and sequence analysis of the evgAS genes involved in signal transduction of Escherichia coli K-12.";
Nucleic Acids Symp. Ser. 27:149-150(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20378313; PubMed=10923791; Kato A., Chnishi H., Yamamoto K., Furuta E., Tanabe H., Utsumi R.; "Transcription of emrKY is regulated by the EvgA-EvgS two-component system in Escherichia coli K-12."; Blosci. Biotechnol. Blochem. 64:1203-1209(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12;
MEDILNE-93149980; PubMed-9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Aiba H., Baba T., Hayashi K., Miki T., Mitsuhashi N.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STARAIN-KIZ / Mulbs5;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                    Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                 Utsumi R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki Nakagawa H., Miwa A., Tanabe H., Noda M.; Weaki Jednifiad genes involved in the signal transduction of Escherichia coli K.12."; Gene 140:73-77(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (VARIANTS EVGS1 AND EVGS4).
                                                                                                                                                                                              EVGS_ECOLI STANDARD: PRT; 1197 AA. P30855; P7764, Q9RF37; P1-11993 (Rel. 26, Created) Ol-WUV-1997 (Rel. 35, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) EvGS OR E2370.
          NARL_ECOLI
CITT_BACSU
CTRA_CAUCR
                                        CPXR_ECOLI
CZCR_ALCEU
RPFC_XANCP
CHEY_THEMA
YC27_PORPU
PILL_PSEAE
ATOC_ECOLI
                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
MEDLINE=94171083; PubMed=8125343;
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581.421 Million cell updates/sec
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                                                                                                                                   1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                      127863 segs, 47026705 residues
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DCTR_BACME
BARA_ECOLI
YSO1_PLEBO
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                  123 | PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
1009 | PHOSPHORYLATION (BY SIMILARITY).
1137 | PHOSPHORYLATION (BY SIMILARITY).
1137 | PHOSPHORYLATION (BY SIMILARITY).
151 | E -> G (IN EVGS1; CONSTITUTIVELY ACTIVE).
152 | E -> G (IN REF. 1 AND 2).
273 | FF -> PH (IN REF. 1 AND 2).
421 | SQ -> FE (IN REF. 1 AND 2).
275 | SQ -> FE (IN REF. 1 AND 2).
276 | SQ -> FE (IN REF. 1 AND 2).
277 | SQ -> FE (IN REF. 1 AND 2).
278 | G -> C (IN REF. 1 AND 2).
279 | G -> D (IN REF. 1 AND 2).
271 | SQ -> FE (IN REF. 1 AND 2).
272 | C -> D (IN REF. 1 AND 2).
273 | G -> D (IN REF. 1 AND 2).
274 | C -> D (IN REF. 1 AND 2).
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STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
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STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; Pubmed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Perna N.T., Plunkett G. III, Burland V., Mau C., Kirkpatrick H.A.,

Rose D.J., Mayhaw G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Davis N.W., Lim A., Shao, Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaco J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
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Enterobacteriaceae; Escherichia.
NCBL_TaxID-83334;
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CYTOPLASMIC (POTENTIAL)
                        HISTIDINE KINASE.
RESPONSE REGULATORY.
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34.4%; Pred. No. 2.9e-07;
ive 25; Mismatches 52
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein evgS precursor (EC 2.7.3.-).
Escherichia coli 0157:H7.
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                                   system evgS/evgA.
in response to
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
MW; A01055089D9618E2 CRC64;
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                                                                                                                                                                                                                                     ij
Res. 8:11-22(2001).
FUNCTION: Member of the two-component regulatory system evgS/evg Phosphorylates evgA via a four-step phosphorelay in response to environmental signals (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                               (Probable).
PTM: Activation requires a sequential transfer of a phosphate prus. Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain and to a His in the secondary transmitter the receiver domain and to a His in the secondary transmitter
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R PRINTS: PRO0344; BETLUARD'S A.

R SMART: SM00387; HAPPase_C; 1.

R SMART: SM00073; HTS. 1.

R SMART: SM00073; HTS. 1.

R SMART: SM00062; PBPD; 2.

R SMART: SM0048 REC; 1.

R SMART: SM0048 REC; 1.

R PROSITE; PS50109; HTS. 1.

R PROSITE; PS50109; HPT; 1.

R PROSITE; PS50100; TRS. 1.

R PROSITE; PS50110; RSPONSE_REGULATORY; 1.

R PROSITE; PS50110; RSPONSE_REGULATORY; 1.

R PROSITE; PS50110; RSPONSE_REGULATORY; 1.

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R PROSITE; PS50110; RSPONSE_REGULATORY; 1.

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                                                                                                                                                                                                                                                                                           domain (By similarity).
--- SIMILARITY: Contains 1 histidine kinase domain.
--- SIMILARITY: Contains 1 HPT domain.
--- SIMILARITY: Contains 1 response regulatory domain.
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Pred. No. 4.3e-07;
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RESPONSE REGULATORY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003594; Arpbind_Arpase.
Interpro; IPR003594; Arpbind_Arpase.
Interpro; IPR003561; His_Kina.
Interpro; IPR005667; His_Kinase.
Interpro; IPR005570; Hpt.
Interpro; IPR001370; Hpt.
Interpro; IPR001311; SBP/glu_receptor.
IPEmm; PP005121; HiskA; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE005468; AAG57495.1; -. EMBL; AP002561; BAB36672.1; -.
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721 721
1009 1009
1137 1137
1197 AA; 134953 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00497; SBP_bac_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A91035; A91035
PIR; C85879; C85879.
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Best Local Similarity
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TRANSMEM
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TRANSMEM
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MOD_RES
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          DNA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                         1013 PNVDGFELTRKLREQNSSLPIWGLTANA-QANEREKGLNCGMNLCLFKPLTLDVLKTHLS 1071
72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2] SEGUENCE FROM N.A. C0031; SEGUENCE FROM N.A. C0031; SEGUENCE FROM N.A. C00931; STRAIN=Ty2 / ATCC 700931; MEDLINE-22331667; PubMed=12644504; MEDLINE-22331667; PubMed=12644504; Medline-2233167; PubMed=12644504; Medline-223316004; Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoylanni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CI18."; and CI18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).
-! - SIMILARITY: Contains 1 histidine kinase domain.
-! - SIMILARITY: Contains 1 PAS (PER-ARNI-SIM) dimerization domain.
-! - SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis.";
J. Bacteriol. 178:1691-1698(1996).
J. Bacteriol. Member of the two-component regulatory system rcsC/rcsB involved in the regulation of the expression of genes involved in the regulation of the expression and genes involved in colanic acid capsule synthesis. RcsC probably functions as a colanic acid capsule synthesis. RcsC probably functions as a membrane-associated protein kinase that phosphorylates rcsB in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response to environmental signals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       948 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=96198173; Pubmed=8626298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                1072 QL 1073
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                                                                                                                                                                                                       132 QL 133
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
W; AE3A21701265A865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SM00448; KEC; 1.

PROSITE; PS50109; HIS.KIN; 1.

PROSITE; PS50110; PAS: FALSE_NEG.

PROSITE; PS50110; RESPONSE_REGULATORY; 1.

Sensory transduction; Transferase; Kinase; Bacterial capsule; Inner membrane; Transmembrane; Phosphorylation; Complete proteome.

CYTOPLAMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Έ
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
5-noor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 948;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.6%; Score 173.5; DB 1; 33.9%; Pred. No. 5.9e-07;
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HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           948 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Mismatches
                                                                                                                                                                                            nastronomy products and proposed interpro; pre003601; his_than.
Interpro; pre003601; his_than.
Interpro; pre003601; his_than.
Interpro; pre003601; his_than.
Interpro; pre001014; pas_domain.
Interpro; pre001014; pas_domain.
Interpro; pre00118; harbase_c; l.
Pfam; pre00218; harbase_c; l.
Pfam; pre00219; response_reg; lem; pre00019; response_reg; l.
Prints; pre0072; response_reg; l.
Prints; pre0073; response_reg; l.
Prints; pre00739; Response_reg; l.
SWART; SM00388; hiskA; l.
SWART; SM00448; REC; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106237 MW;
                                                                                                                   EMBL, AL627274; CAD07502.1; -. EMBL; AE016836; AA068299.1; -. EMBL; X87830; CAA61095.1; -. HSSP; P06143; LUDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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nes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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RCSC OR STM2271.
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STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-2153448; PubMed-11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille'P')
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Probable).
--- PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).
--- SIMILARITY: Contains 1 histidine kinase domain.
--- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
--- SIMILARITY: Contains 1 response requiatory domain.
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                                                                                                                                                                                                                                                         Nature 41:3824806(1001).

-i- FUNTION: Member of the two-component regulatory system rcsC/rcsB
-i- FUNTION: Member of the two-component regulatory system rcsC/rcsB
involved in the regulation of the expression of genes involved in
colanic acid capsule synthesis. RcsC probably functions as a
membrane-associated protein kinase that phosphorylates rcsB in
response to environmental signals.

-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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HESPONSE REGLATORY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

106279 MW; BAAD8DA557D5868B CRC64;
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Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Simplete genome sequence of Salmonella enterica serovar Typhimurium
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SMART; SM00387; HATPASe_C; 1.
SMART; SM00388; HISKA; 1.
SMART; SM00448; REC; 1.
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                                                                                                     EMBL; M28242; AAA24503.1; ALT_INIT.
EMBL; L11272; AAA24505.1; ALT_INIT.
EMBL; ABC003311; AAC75278.1; ALT_INIT.
EMBL; D90850; BAA16001.1; ALT_FRAME.
EMBL; D90850; BAA16006.1; ALT_FRAME.
EMBL; D90851; BAA16009.1; ALT_FRAME.
EMBL; D90851; BAA16014.1; ALT_FRAME.
ENGL; D90851; BAA16014.1; ALT_FRAME.
ECGGENE; EG10822; rcsC.
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                                                                                                                                                                                                                                             interPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003594; Bact_sens_pr_C.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR00467; His_kinas.
InterPro; IPR001467; His_kinase.
InterPro; IPR001789; Response_reg.
Fam; PF00518; HATPase_c; 1.
Pfam; PF00512; HisKa; 1.
Pfam; PF00512; HisKa; 1.
Pfam; PF00012; Response_reg; 1.
Prints; PF00044; BCTRLSENSOR.
Probom; PD000039; Response_reg; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Kaaai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mixi T., A Kaai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mixi T., A Macobuchi K., Mori H., Makaba S., Nakamura Y., A Nashimoto H., Nishio Y., Oshima T., Santo N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Tamanoto Y., Holuchi T., T., Takeda J., Takemoto K., Wada C., Tamanoto Y., Holuchi T., T., Takeda J., Takemoto K., Wada C., Tamanoto Y., Holuchi T., T., Takeda J., Takemoto K., Wada C., Takemoto T., Pola Sequence of the Corresponding to the 40.1-50.0 min region on the linkage map.";

I. DNA Res. 31379-324(1996).

I. DNA Res. 31379-324(1996).

I. PUNCTION: Member of the two-component regulatory system rcsC/rcsB collaric acid capsule synthesis. ResC probably functions as a membrane-associated protein kinase that phosphorylates rcsB in response to environmental signals.

I. SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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-i. SIMILARITY: Contains I histidine kinase domain.
-i. SIMILARITY: Contains I PAS (PER-ARNT-SIM) dimerization domain.
-i. SIMILARITY: Contains I response regulatory domain.
-i. CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of rcsB and rcsC from Escherichia coli 09:K30:H12 and examination of the role of the rcs regulatory system in expression of group I capsular polysaccharides.";
J. Bacteriol. 175:5384-5394(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                   Stout V., Gottesman S.;
"RcsB and RcsC: a two-component regulator of capsule synthesis in
Escherichia coli.";
                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                           RCSC_ECOLI STANDARD; PRT; 949 AA.
P14376; P76457; P97170; P97202; Q47586;
01-JAN-1990 (Rel. 13, Created)
28-FBB-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                Jayaratne P., Keenleyside W.J., Maclachlan P.R., Dodgson C., Whitfield C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                                                  MEDLINE-90130299; PubMed-2404948;
                                                                                                                                                                                                                                                                                                                                                Bacteriol, 172:659-669(1990).
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                                                                                                                                                                           Escherichia coli.
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                                                                                                                                                                                                                                                                      STRAIN=K12
                                                                                                                                          component
             RESULT 5
RCSC_ECOLI
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         940 RESPONSE REGULATORY

940 RESPONSE REGULATORY

945 PHOSPHORYLATION (AUTO-) (BY SIMILAR

945 PHOSPHORYLATION (BY SIMILARITY).

315 L -> V (IN STRAIN 09:K30:H12).

946 L -> V (IN STRAIN 09:K30:H12).

948 L -> V (IN STRAIN 09:K30:H12).

948 L -> V (IN STRAIN 09:K30:H12).

948 D -> E (IN STRAIN 09:K30:H12).

948 D -> E (IN STRAIN 09:K30:H12).

948 T -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00387; HATPESE_C: 1.
SMART; SM00388; HisKA: 1.
SMART; SM00019; PAS; 1.
PROSITE; PS50109; HIS_KIN: 1.
PROSITE; PS50112; PAS; PALSE_NEG.
PROSITE; PS50112; PAS; PALSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Bacterial capsule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.3%; Score 171.5; DB 1; Length 949; 33.9%; Pred. No. 8.6e-07; ive 32; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
FRZE_MYXXA STANDARD; I
AC PRZE_MYXA STANDARD; I
DT 01-NOV-1990 (Rel. 16, Created)
```

9

3

Gaps

ι, ..

35.2%; Pred. No. 1.2e-05; ive 27; Mismatches 38; Indels

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Best Local Similarity 35.2
Matches 38; Conservative
                                                           qq
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                                                                                                                 qq
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                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
ALA/PRO-RICH (POSSIBLE HINGE REGION).
9912BD40991C69E5 CRC64;
                                                                                                                                       MCCleary W.R., Zusman D.R.;
"FrzE of Myxococcus xanthus is homologous to both CheA and CheY of Salmonella typhimurium.";
                                                              Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
NCBL_TaxID=34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS5081, CHEW, 1.
PROSITE: PS50109; HIS_KIN; 1.
PROSITE: PS501094 HIS_KIN; 1.
PROSITE: PS5084; HIPT; 1.
PROSITE: PS501010; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation.
01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Gliding motility regulatory protein (EC 2.7.3.-).
                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 87:5898-5902(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESPONSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HISTIDINE KINASE.
CHEW-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP: Q56310; 1B3Q.
Interpro; PR003594; ATPbind_ATPase.
Interpro; IPR003595 Bact_sens_pr_C.
Interpro; IPR003456; CheW.
Interpro; IPR00367; H1s_kinase.
Interpro; IPR003767; Hpt.
Interpro; IPR001789; Response_reg.
Ffam; PF01584; CheW; 1.
Pfam; PF02518; Hpt; 1.
Pfam; PF00518; Tesponse_reg; 1.
Pfam; PF0072; response_reg; 1.
Pfam; PF0072; response_reg; 1.
Prns; PR00072; response_reg; 1.
Prns; PR00073; Hpt; 1.
SWART; SW00260; CheW; 1.
SWART; SW00073; HPT; 1.
                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE=90332690; PubMed=2165608;
                                                                                                                                                                                                                        MEDLINE=91072208; PubMed=2123853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M35192; AAA25396.1; -.
                                                                                                                                                                                                [2]
PHOSPHORYLATION OF HIS-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A35966; A35966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 1777 AA;
                                                   Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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MOD_RES
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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Score 156.5; DB 1; Length 777;

23.1%;

Query Match

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                        14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-94042854; PubMed=8226633;
Brown J.L., North S., Bussey H.;
"SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
"SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
beta-glucan assembly, encodes a product with domains homologous to
prokaryotic two-component regulators and to heat shock transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Jöhnston L., Langskon Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St.Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95045411; Pubmed-7957083;
Brown J.L., Bussey H., Stewart R.C.;
"Yeast Skn7p functions in a eukaryotic two-component regulatory
                                                                                                  74 RDGVSTTKKLREMEVKSMI - - VGVTSLADNEEERRAFMEAGLNHCLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krems B., Charizanis C., Entian K.-D.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCECLULAR LOCATION: Nuclear.
SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                             SKNT_YEAST STANDARD; PRT, 622 AA. P18889; P3889; P3747, 01.FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-FEB-1995 (Rel. 41, Last annotation update) Putative transcription factor SkN7 (PoS9 protein). SKN7 OR POS9 OR BRY1 OR YHR206W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 175:6908-6915(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factors."
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DOMAIN
      69 KEMPERDGVSTIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI-- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECRETAR OLD: THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CON
            EMEL; U00485; AAC48911.1; -
REMEL; U00485; AAC48911.1; -
REMEL; W3331; CAA58143.1; -
REMEL; W3331; CAA58143.1; -
REMEL; W3334; AAC48344.
R HSSP, P22121; ZHTS.
R HSSP, P22121; ZHTS.
R TRANSFAC; T03481; -
R SGD; S0001249; SKN. -
R GO; GO:0005649; C:nucleus; IDA.
R GO; GO:000156; F:transcription factor activity; IDA.
R GO; GO:000166; F:transcription; IDA.
R GO; GO:000169; P:transcription; IDA.
R InterPro; IPR00232; HSF_DNA_bind.
R InterPro; IPR00139; Response_reg.
R InterPro; IPR00139; Response_reg.
R Fiam; PP00447; HSF_DNA_bind.
R Pfam; PP00447; HSF_DNA_bind; I.
R Pfam; PP00472; HSF_DNA_bind; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRODON: PRODOSS, HSPDOMAIN.
Prodon: PRO01788: HSPDOMAIN.
Prodon: PD001788: HSPDOMAIN.
Prodon: PD001788: HSPDOMAIN.
Prodon: PD001788: HSPDOMAIN.
SMART: SM00448; REC; 1.
SMART: SM00448; REC; 1.
SMART: SM00448; REC; 1.
PROSITE: PS50110; RESPONSE_REGULATORY; 1.
Transcription requisition: Sensory transduction; Nuclear protein; DNA-binding: Phosphorylation.
DNA-binding: Phosphorylation.
BNA-BIND 86 190 RESPONSE REGULATORY.
MOD_RES 427 427 PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Aerobic respiration control sensor protein arcB (EC 2.7.3.-).
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.1%; Score 150; DB 1; Length 622; 28.1%; Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 492 RESPONSE REGULATORY.
427 427 PHOSPHORYLATION (PROBABLE).
427 427 D-N: DIMINISHED ACTIVITY.
427 427 D-NE AUGMENTED ACTIVITY.
622 AA, 69202 MW, 4C732FD66E326742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----1PLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 ILIRYLKDRIPLCEQ 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARCB_ECO57
ID ARCB_ECO57
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Best Local (
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MOD_RES
MUTAGEN
MUTAGEN
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RECORDENCE FROM N.A.

SEQUENCE FROM N.A.

RA Hayashi T. Makino K., Ohisibi M., Murckawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Shiba T., Hattori M., Shinagawa H.;

RA Kulara S., Shiba T., Hattori M., Shinagawa H.;

RA Romplete genome sequence of enterohemorrhagic Escherichia coli

FRI "Complete genome sequence of enterohemorrhagic Escherichia eroli

FRI "Complete genome sequence of enterohemorrhagic Escherichia archia archia for anaerobic repression of the arc

sensor-regulator protein for anaerobic repression of the arc

modullon. Activates arch via a four step phosphorelay. ArcB can

also dephosphorylate arch via a four step phosphorelay involving His-

CC "INTERNA" LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain (By similarity).
-: SIMILARITY: Contains 1 histidine kinase domain.
-: SIMILARITY: Contains 1 HPT domain domain.
-: SIMILARITY: Contains 1 PAS (PBR-ARNT-SIM) dimerization domain.
-: SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
-: SIMILARITY: Contains 1 response regulatory domain.
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             group from a His in the primary transmitter domain, to an Asp
the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: Activation requires a sequential transfer of a phosphate
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Sensory transduction; Transferase; Kinase; Phosphorylation;
Transmembrane; Inner membrane; Transcription regulation;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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PIR, AP002564, BAB37512.1; --
PIR, DBS985, DB5985.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003661; His_Kina.
InterPro; IPR003661; His_Kina.
InterPro; IPR0003661; His_Kina.
InterPro; IPR000700; PAS-assoc_C.
InterPro; IPR0010700; PAS-assoc_C.
InterPro; IPR00114; PAS_domain.
InterPro; IPR001189; Response_req.
Pfam; PF00312; HATPase_C; 1.
Pfam; PF00312; HisKa; 1.
Pfam; PF00072; response_req; 1.
ProDom; PD000039; Response_req; 1.
SWART; SW00387; HATPase_C; 1.
SWART; SW00031; HATPASE_C; 1.
SWART; SW00031; HATPASE_C; 1.
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PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50894; HPT; 1.
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PROSITE; PS50113; PAC; 1.
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DOMAIN 1
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MEDLINE=90355832; PubMed=2201868;
Iuchi S., Matsuda Z., Fujiwara T., Lin E.C.C.;
"The arcB gene of Escherichia coli encodes a sensor-regulator protein
for anaerobic repression of the arc modulon.";
Mol. Microbiol. 4:715-727(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G. Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                        LNVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD
                                                                                                                     3; Gaps
                                               PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECIES-E.coli, STRAIN-K12 / MG1655;
SPECIES-E.coli, STRAIN-K12 / MG1655;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shoo Y.
                                                                                                                                                                                                                                                                                                                                                                       Shigella flexneri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae; Escherichia.
                                                                                                 DB 1; Length 778;
                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
15-5EB-2003 (Rel. 42, Last annotation update)
Aerobic respiration control sensor protein arcB (EC 2.7.3.-).
ARCB OR B3210 OR SF3250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                     Indels
                                                                              C8AE004B007F9D30 CRC64;
PAS.
PAC.
HISTIDINE KINASE.
RESPONSE REGULATORY.
HPT.
                                                                                                          ; Pred. No. 4.6e-05; 40; Mismatches 47;
                                                                                                                                                                                                                                                                                           778 AA.
                                                                                             22.1%; Score 149.5;
25.6%; Pred. No. 4.6
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                                                                              88010 MW;
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Best Local Similarity 25.6%
Matches 31; Conservative
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778 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rato M., Mizuno T., Hakoshima T.;
"Crystallization of a complex between a novel C-terminal transmitter,"
HPt domain, of the anaerola sensor kinase ArcB and the chemotaxis response regulator CheY.";
                                                                                                                                                                                                                                                                SPECIES-E.COLI, STRAIN-M15;
MEDLINE-99047671; PubMed-9830034;
Georgellis D., Kwon O., De Wulf P., Lin E.C.C.;
"Signal decay through a reverse phosphorelay in the arc two-component signal transduction system.";
J. Biol. Chem. 273:32864-32869(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS OF HIS-292; ASP-576 AND HIS-717.
SPECIES-E.coli; STRAIN=K12 / MC4100;
MEDLINE=20309722; PubMed=10851007;
Kwon O., Georgellis D., Lin E.C.C.;
Phosphorelay as the sole physiological route of signal transmission by the arc two-component system of Escherichia coli.";
J. Bacteriol. 182:3858-3862(2000).
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-:- SIMILARITY: Contains 1 HPT domain.
-:- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-:- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
-:- SIMILARITY: Contains 1 response regulatory domain.
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-!-PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=E.col;

MEDLINE=97207018; PubMed=9054511;

Kato M., Mizuno T., Shimizu T., Hakoshima T.;

"Insights into multistep phosphorelay from the crystal structure

the C-terminal HPt domain of ArcB.";

Cell 88:717-723(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 659-776 IN COMPLEX WITH
SPECIES=E.coli; STRAIN=M15;
MEDLINE=97431492; PubMed=9286997;
Georgellis D., Lynch A.S., Lin E.C.C.;
In vitro phosphorylation study of the arc two-component signal transduction system of Escherichia coli.";
J. Bacteriol. 179:5429-5435(1997).
(5)
CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS) OF 660-778
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MEDLINE=20003135; PubMed=10531481;
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SLN1_YEAST
P39928;
RESULT 10
SLN1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART: SM00073; HPT: 1.
SMART: SM00073; HPT: 1.
SMART: SM00073; HPT: 1.
SMART: SM000073; HPT: 1.
SMART: SM000073; HPT: 1.
TIGRFAMS: TIGR00229; sensory_box: 1.
TIGRFAMS: TIGR00229; sensory_box: 1.
TIGRFAMS: TIGR00229; sensory_box: 1.
PROSITE: PS50109; HIS_KIN: 1.
PROSITE: PS50113; PAS: 1.
PROSITE: PS50113; PAS: 1.
PROSITE: PS50110; RESPONSE_REGULATORY: 1.
Sensory transduction: Transferase; Kinase; Phosphorylation;
Transmembrane; Inner membrane; Transcription regulation; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.1%; Score 149.5; DB 1; Length 778; 25.6%; Pred. No. 4.6e-05; ive 40; Mismatches 47; Indels 3;
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PHOSPHORYLATION (PROBABLE).
PHOSPHORYLATION (PROBABLE).
H->Q: LOSS OF ACTIVITY.
D->A: LOSS OF ACTIVITY.
H->Q: LOSS OF ACTIVITY.
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RESPONSE REGULATORY.
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                                                                                                                     PLE: JAOB: 18-MAR-98
PDB: JAOB: 18-MAR-98
PDB: JAOB: 17-JUN-98
PDB: JERU; 31-DEC-02
PDB: JERU; 31-DEC-02
ECGENCE: EGIOGE2; arcal
InterPro: JERRO03594; ATPbind_ATPase.
InterPro: JERRO03594; ATPbind_ATPase.
InterPro: JERRO03504; His_kinase.
InterPro: JERRO03507; Hpt.
InterPro: JERRO03507; Hpt.
InterPro: JERRO0700; PAS-asco._C.
InterPro: JERRO01709; PAS-asco._C.
InterPro: JERRO01709; RAS-asco._C.
InterPro: JERRO01709; RAS-asco._C.
InterPro: JERRO01709; RAS-asco._C.
InterPro: JERRO01709; RAS-asco._C.
Ffam: PPO0512; HATPASSE._C; 1.
Pfam: PPO0909; PAS; 1.
Pfam: PPO09044; BCTRLEENOR.
PRINTS: PRO0344; BCTRLEENOR.
PRODON: JERRO0349; BCTRLEENOR.
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                      EMBL; U18997; AAADOULL.,
EMBL; AE000400; AAC76242.1; --
EMBL; AE015336; AAN44715.1; --
PIR; D65112; RGECAR.
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RESULT 12
GACS_PSESY
   SOUTH THE FEET OF SOUTH THE SOUTH TO SOUTH THE
  DA PP
   q
   ò
   Q
   ò
   Db
  9
   1136 ENYNMIFMDVQMPKVDGLLSTKMIRRDLGYTSPIVALTAFADDSNIKEC-LESGMNGFLS 1194
   60 SSFDLILMDKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLA 118
   8 DIEKIKKKLNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG 59
  44; Indels 14; Gaps
   RESPONSE REGULATORY.
PHOSPHORYLATION (AUTO-) (PROBABLE).
PHOSPHORYLATION (PROBABLE).
N-LINKED (GLCNAC...) (POTENTIAL).
  SEQUENCE FROM N.A., AND MUTAGENESIS.
MEDLINE=94239408; PubMed=8183345;
Maeda T., Wurgler-Murphy S.M., Saito H.;
"A two-component system that regulates an osmosensing MAP kinase cascade in yeast.";
Nature 369:242-245(1994).
   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
  H->Q: INACTIVE.
G->D: SLOW GROWTH, SLN1-1 MUTANT.
D->N: INACTIVE.
  Score 145; DB 1; Length 1220; Pred. No. 0.00018;
  PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation;
   AA; 134434 MW; 45FFE24A8165486B CRC64;
   POTENTIAL.
EXTRACELLULAR (POTENTIAL).
   CYTOPLASMIC (POTENTIAL). HISTIDINE KINASE.
  CYTOPLASMIC (POTENTIAL).
  SSKI_YEAST STANDARD; PRT; 712 AA. 007084; 007909; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 0somolarity_two-component system protein SSK1
  40; Mismatches
   PRINTS; PR00344; BCTRLSENSOR.
ProDom; PD000039; Response_reg; 1.
  [2]
SEQUENCE FROM N.A.
SIRALINE-S288c / AB972;
MEDLINE-97313267; Pubmed-9169871;
  1195 KPIKRPKLKTILTEFCAA 1212
                             PF00072; HiskA; 1.
PF00072; response_reg; 1.
   KPLTKDKIIPLINQLMDA 136
   21.4%;
29.0%;
   SWART; SM00387; HATPASE_C; 1
SWART; SM00388; HiSKA; 1.
SWART; SM00448; REC; 1.
PF02518; HATPase_c; 1.
  40; Conservative
   Query Match
Best Local Similarity
   SSK1 OR YLROOGC.
  NCBI_TaxID=4932;
   Transmembrane.
DOMAIN
TRANSMEM 2
DOMAIN 4
TRANSMEM 333
   CARBOHYD
CARBOHYD
CARBOHYD
   DOMAIN
MOD_RES
MOD_RES
   SEQUENCE
  CARBOHYD
  CARBOHYL
  MUTAGEN
  DOMAIN
   MUTAGEN
  Matches
DORNAL PETER
   qq
  셤
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A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Bentan K.-D., Flocath M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Nortweller-Auer S., Nentwich U., Obermaler B., Piravandi E., Pohl T.M., A Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Unestvoad A.P., Urestarazu L.A., Vandenbol M., Varhassell F., Medler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; The nucleotide sequence of Saccharomyces cerevisiae chromosome XII. T., The nucleotide sequence of Saccharomyces cerevisiae chromosome XII. T., Nature 387:87-90(1997).

1. FUNCTION: FORMS PART OF A TWO-COMPONENT REGILATORY SYSTEM SINIARS STAL/SERZ2-PROGI PATHWAY. THE UNPROSHORYTROE THE SYSZ/SERZ2-PROGI PATHWAY. THE UNPROSHORYTROE STEM STAL/SERZ2-PROGI PATHWAY. THE UNPROSHORYTROE STEM STAL/SERZ2-PROGI PATHWAY. THE UNPROSHORYTREE STHMULATE THE PBS2-HOGI MAPKKE THAY FURTHER STHMULATE THE PBS2-HOGI MAPKKE THAY FURTHER STHMULATE THE PBS2-HOGI MAPKME MAPKKE THAY FURTHER STHMULATE THE PBS2-HOGI MAPKME MAPKMES AND SERZA MAPKMES AND S
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  556 OLPVLSGIEAAKOIRDFEKONGIGIOKSLNNSHSNLEKGTSKRFSQAPVIIVALTASNSQ 615
  70 EMPERDGVSTTKKLREMEVKS------101
  SGD; SG003996; SSK1.
GO; GO:0007234; P:osmosensory signaling pathway via two-compo. . .; IDA.
GO; GO:0042542; P:response to hydrogen peroxide; IMP.
InterPro; IPR001789; Response_reg.
Pfam; PF00072; response_reg.
  10 EKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDK
   21.2%; Score 143.5; DB 1; Length 712; 27.9%; Pred. No. 0.00013;
   Indels
  PHOSPHORYLATION (PROBABLE).
   - FUGSTRUATION TO TWIENDER WITH SSK2 AND SSK22.
-- SUBGELITAR LOCATION: Cytoplasmic (Potential).
-- SIMILARITY: Contains 1 response regulatory domain.
   D->N: ACTIVATES.
P -> S (IN REF. 1).
; 33B2DBB4FCF2528A CRC64;
   RESPONSE REGULATORY
   907 AA
   GACS_PSESY STANDARD; PRT; 907 AA P48027; 01-FB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update)
   28; Mismatches
  Probon; PD000039; Response_reg; 1.
SMART; SM00448; REC; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Phosphorylation.
DOMAIN 505 647
   102 EEERRAFMEAGLNHCLAKPL 121
   616 MDKRKALL-SGCNDYLTKPV 634
   78529 MW;
  EMBL; L26523; AAA35100.1; -. EMBL; Z73178; CAA97528.1; -. PIR; S64828; S64828.
   Conservative
   181
712 AA;
   Similarity
  Query Match
Best Local Simi
Matches 39;
  MOD_RES
MUTAGEN
CONFLICT
SEQUENCE
```

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284 2
707 7
853 8
   NCBI_TaxID=1423;
   STRAIN=168;
  Bacteria;
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
  DCTR_BACSU
  RESULT 13
   FT
FT
SO
   g
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   ò
  Q
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   PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp in the receiver domain and to a His in the secondary transmitter
   SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
  R HSSP, P06143; 1UDR.

A INTEPPO: IPR003594; AIPbind_ATPase.

A InterPro; IPR003569; Bact_sens_pr_C.

A InterPro; IPR003669; HAMP.

A InterPro; IPR003669; HAMP.

A InterPro; IPR003669; HAMP.

A InterPro; IPR003669; HAMP.

A InterPro; IPR001799; Response_reg.

B Pfan; PF00512; HAMP; 1.

R Pfan; PF00512; HAMP; 1.

R Pfan; PF00512; HAMP; 1.

R Pfan; PF00512; HAMP; 1.

R Pfan; PF00349; Response_reg; 1.

R Pfan; PF00344; BAMP; 1.

R SMART; SM00344; BAMP; 1.

R SMART; SM00387; HATPase_c; 1.

R SMART; SM00389; HAMP; 1.

R SMART; SM00448; REC; 1.

R R SMRT; SM00448; REC; 1.

R R SMRT; SM00448; REC; 1.

R R PROSITE; PS50894; HAMP; 1.

R PROSITE; PS50894; HAMP; 1.

R PROSITE; PS50894; HAMP; 1.

R PROSITE; PS50894; HPT; 1.

R PROSITE; PS50804; HAMP; 1.
   Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
   domain (By similarity).
-- SIMILARITY: Contains 1 HAMP domain.
-- SIMILARITY: Contains 1 histidine kinase domain.
-- SIMILARITY: Contains 1 HPT domain.
-- SIMILARITY: Contains 1 response regulatory domain.
   HISTIDINE KINASE.
RESPONSE REGULATORY.
HPT.
28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein gacs (EC 2.7.3.-).
GACS OR LEMA.
   POTENTIAL.
POTENTIAL.
HAMP.
   POTENTIAL.
  [1]
SEQUENCE FROM N.A.
MEDLINE=92234961; PubMed=1314807;
Hrabak E.M., Willis D.K.;
  Inner membrane.
  Pseudomonadaceae; Pseudomonas
  EMBL; M80477; AAA25877.1; -. HSSP; P06143; 1UDR.
  Transmembrane;
TRANSMEM 9
TRANSMEM 84
  (Probable).
  NCBI_TaxID=321;
   TRANSMEM
   DOMAIN
   DOMAIN
THE FIRM WANDERS RESERVED BY A
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Kunst E., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borliss R., Boursier L., Brans A., Braun M., Brignells Z.C., Bron S.,
Broulllet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Filtz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RHIbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita R., Lapidus A., Lardinots S., Lauber J., Lazarevic V.,
RA Kurita R., Lapidus A., Lardinots S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Reger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Serowska A., Seror S.J., Serror P., Shin B.S.,
RA Schiguchi J., Serwoska A., Serror P., Shin B.S.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Hosato W., Uchiyama S., Vandenbol M., Vanier P., Vasta K.,
RA Viari A., Wambutt R., Wadler E., Wedler H., Yasumoto K., Yata K.,
RA Viari A., Wambutt R., Yamamoto H., Yamane R., Yoshikawa H.F., Zumstein E., Yoshikawa H., Pakenden R.,
Roshika W., Waller B., Roche B., Yoshikawa H., Danchin A.,
Roshika W., Waller B., Roche B., Yoshikawa H., Nandel B., Yoshikawa H.F., Zumstein E., Yoshikawa H., Yoshikawa H.F., Zumstein E., Yoshikawa H., Yoshikawa H., Yoshikawa H., Yanganga D., Yoshikawa H., Yanganga D., Yoshikawa H., Yanganga D., Yanga K.,
   69 KEMPERDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTK 123
  18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGG------SSFDLILMD 68
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
FROSPHORYLATION (BY SIMILARITY).
5B9F4663DAF3492C CRC64;
  Rasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
"A 148 kbp sequence of the region between 35 and 47 degree of
Bacillus subtilis genome.";
   20.9%; Score 142; DB 1; Length 907; 27.6%; Pred. No. 0.00023; Live 33; Mismatches 33; Indels
   Bacillus subtilis genome.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
   Firmicutes; Bacillales; Bacillaceae; Bacillus.
   DCTR_BACSU STANDARD; PRT; 226 AA.
P96602; P94503;
16-0CT-2001 (Rel. 40, Created)
16-0CT-CRE-2003 (Rel. 41, Last annotation update)
Probable C4-dicarboxylate response regulator dctR.
  MEDLINE-98044033; PubMed-9384377;
  99195 MW;
  Query Match 20.9%
Best Local Similarity 27.6%
Matches 35; Conservative
    284
707
853
  124 DKIIPLI 130
  767 RQLAQVV 773
  SEQUENCE FROM N.A.
  [2]
SEQUENCE FROM N.A.
STRAIN-168;
   Bacillus subtilis.
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us-09-646-679-15\_1.rsp

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Probable C4-dicarboxylate response regulator dctR.
  PD000039; Response_reg; 1.
  EMBL; AP001516; BAB06470.1; -.
  Bacteria; Firmicutes;
NCBI_TaxID=86665;
  SEQUENCE FROM N.A.
STRAIN=168 / OI1085;
                              Bacillus halodurans.
Bacteria, Firmicutes
  PIR; G83993; G83993.
HSSP; P10957; 1RNL.
   NCBI_TaxID=1423;
  CHEY_BACSU
         δ
   q
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  ద
  13 KKKLNVLIVDDDPLNLIIHEKIIKAIGGIS--QTANNGEEAVIIHRDGGSSFDLILMDKE 70
   71 MPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.",
  MEDCINE-20170658; PubMed-10708364; MEDCINE-20170658; PubMed-10708364; Asai K., Baik S.-H., Kasahara Y., Moriya S., Ogasawara N.; Regulation of the transport system for C4-dicarboxylic acids in
   .;
2
  Probon, PD000039, Response_reg; I.

SMART; SM0446, REC; I.

PROSITE; PS50110; RESPONSE_REGULATORY; I.

PROSITE; PS50110; Transcription regulation; DNA-binding;
Activator; Phosphorylation; Complete proteone.

ACINATIN 7 123 RESPONSE REGULATORY.

MOD_RES 58 B PHOSPHORYLATION (BY SIMILARITY).

DNA_BIND 176 206 HFT-H MOTIF (POTEWITAL).

CONFLICT 24 F -> I (IN REF. 3).

SEQUENCE 226 AA; 25539 MW; 018115B14E9ER47D CRC64;
  20.7%; Score 140.5; DB 1; Length 226; 25.9%; Pred. No. 6.7e-05; ive 39; Mismatches 42; Indels 5
  Morel-Deville F., Ehrlich S.D., Morel P., Indentification by PCR of genes encoding multiple response regulators.";
   Last sequence update)
Last annotation update)
   EMBL, 299106; CAB12253.1; --
EMBL, 102580; AAB47751.1; --
FIR B69771; B69771.
FISP, Q56312; 1TMY.
Subtilist; B612074; dctR.
Interpro; IPR001789; Response_reg.
Pfan: PP00072; response_reg. 1.
PIRSF; PIRSF006171; RR_citrat_malat; 1.
  MEDLINE-97311990; PubMed-9168601;
  Microbiology 143:1513-1520(1997).
   (Rel. 40, Created)
(Rel. 40, Last sequ
(Rel. 41, Last anno
   EMBL; AB001488; BAA19283.1; -.
  SEQUENCE OF 14-101 FROM N.A.
  30; Conservative
                                     Nature 390:249-256(1997).
  STANDARD;
   FUNCTION, AND GENE NAME.
   Similarity
  16-OCT-2001
16-OCT-2001
28-FEB-2003
  DCTR_BACHD
Q9K998;
   Query Match
   Best Local
  RESULT 14
DCTR_BACHD
ID DCTR_BA
AC 029K998;
DT 16-OCT-
DT 16-OCT-
DT 28-FEB-
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  16 ENVLIVDDDPLNLIHEKIIKAIGG - · ISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
   74 RDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQ 132
  Gaps
   SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
HOTIKOSHI K.;
   PROSTIE; PSSSIIO; RESPONSE_REGULATORY; 1.
Sensory transduction; Transcription regulation; DNA-binding;
Activator; Phosphorylation; Complete profesome.
DOMAIN 8 124 RESPONSE REGULATORY.
MOD_RES 59 FHOSPHORYLATION (BY SIMILARITY).
DNA_BIND 183 209 H-T-H MOTIF (POTENTIAL).
SEQUENCE 230 AA; 26376 MW; 06FD65F46FC57D40 CRC64;
   Length 230;
   Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Bacillales; Bacillaceae; Bacillus.
   Query Match 20.7%; Score 140.5; DB 1; Best Local Similarity 29.4%; Pred. No. 6.9e-05; Matches 35; Conservative 32; Mismatches 47;
   CHEY_BACSU STANDARD; PRT; 119 AA. P24072; P3783; 101-WAR-1992 (Rel. 21, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 28-PEB-2003 (Rel. 41, Last annotation update) CHEPY OR CHEBY OR CHEBY
   InterPro; IPR00179; Response_reg.
Pfam; PF00072; response_reg; 1.
PIRSF; PIRSF006171; RR_citrat_malat; 1.
ProDom; PD000039; Response_reg; 1.
```

64

Matches

g δ

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chemotaxis.";
J. Biol. Chem. 266:12301-12305(1991).
   Bacteriol. 174:4017-4025(1992).
                       MEDLINE=98044033; PubMed=9384377;
  SEQUENCE OF 95-119 FROM N.A.
  Nature 390:249-256(1997).
   SEQUENCE OF 1-7 FROM N.A.
                  SEQUENCE FROM N.A.
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Search completed: August 13, 2003, 19:11:30 Job time : 12 secs
  32;
   SEQUENCE
  Query Match
  MOD_RES
  Matches
   δ
g
   -!- SUBCELLULAR LOCATION CYtoplasmic.
-!- SIMILARITY: Contains 1 response regulatory domain.
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  MEDLINES 29044035; Funned 93841/;

A Kunst F., Ogaaawara N., Mosser I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

A Borriss R., Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Brillan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Rollseppi G., Guy B.J., Haga K., Galigrily B.J., Grandi G.,

A Guiseppi G., Guy B.J., Haga K., Haicoth J., Harwood C.R., Henaut A.,

Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Guiseppi G., Guy B.J., Haga K., Haicoth J., Harwood C.R., Henaut A.,

Hilbert H., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

A Kurita K., Lardinois S., Lauber J., Lazarevic V.,

A Medina M., Mellado R.P., Mizuno M., Moestl D., Madai S., Mobock M.,

Moone D., O'Reilly M., Ogawa R., Ogiwara A., Oudega B., Park S.H.,

Prescan E., Puilu H., Masuda S., Mauel C., Madique C.,

Medina D., O'Reilly M., Ogawa R., Ogiwara A., Oudega B., Park S.H.,

Prescan E., Puilu F., Mornelle B., Roche B., Rocke M., Sadale Y.,

Prescan E., Puilo P., Purnelle B., Roche B., Rocke M., Sadale Y.,

Prescan E., Puilo P., Purnelle B., Roche B., Rock M., Sadale Y.,

Prescul M., Tamakoshi A., Seros S., Schrocter R., Scoffone F.,

Seriguchi J., Sekowska A., Seros S., Schrocter R., Sondo B.,

Tosato V., Uchiyama S., Vandenbol M., Vaniner F., Vassarotti A.,

Viarl A., Wambutt R., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

Whiters P., Wibhikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

Wattern S., Schleich E., Wedler E., Wedler H., Yoshikawa H., Bonchin A.;

The complete genome sequence of the Gram-positive bacterium Bacillus
   SEQUENCE OF 1-12.

STRAIN=168 / JE642;

MEDLINE=96345629; PubMed=8755892;

MEDLINE=96345629; PubMed=875692;

Graumann P., Schroeder K., Schmid R., Marahiel M.A.;

"Cold shock stress-induced proteins in Bacillus subtilis.";

J. Bacteriol., 178:4611-4619(1996).

I. PUNCTION: HAS A CENTRAL CONTROLLING ROLE IN CHEMOTAXIS. ALTHOUGH

IT IS HOMOLOGOUS TO THE CHEY PROTEIN OF OTHER BACTERIA, IT IS

THOUGHT TO FUNCTION IN A DIFFERENT MANNER.
MEDLINE-91286247; PubMed-1905718; Baschoff D.S., Ordal G.W. "Sequence and characterization of Bacillus subtilis CheB, a homolog of Escherichia coli CheY, and its role in a different mechanism of
  STRAIN=168 / OI1085;
MEDLINE=93078625; PubMed=1447979;
Bischoff D.S., Ordal G.W.,
Identification and characterization of FliY, a novel component of the Bacillus subtilis flagellar switch complex.";
MOI. Microbiol. 6:2715-2723(1992).
   STRAIN=168 / OI1085;
MEDLINE=9228375; PubMed=1597417;
Bischoff D.S., Weinreich M.D., Ordal G.W.;
"Nucleotide sequences of Bacilius subtilis flagellar biosynthetic genes flip and fliQ and identification of a novel flagellar gene,
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   18 VLIVDDDP-LNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG 76
  77 VSTIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQLMD 135
   PROSITE; PS50110; RECY 1.
Chemotaxis; Sensory transduction; Phosphorylation; Complete proteome.
INIT_MET 0 0
  0 0 RESPONSE REGULATORY.
1 118 RESPONSE REGULATORY.
53 53 PHOSPHORYLATION (BY SIMILARITY).
119 AA; 13178 MW; F3BCAOFO2CAB7531 CRC64.
  19.8%; Score 134; DB 1; Length 119; 26.9%; Pred. No. 0.00012; tive 36; Mismatches 47; Indels
   HSSP, Q56312; 1TMY.
Subtilist; BG10258; cheY.
InterPro; IPR001789; Response_reg.
  Pfam, PF00072; response_reg; 1.
Probom, PD000039; Response_reg; 1.
SMART; SM00448; REC; 1
  EMBL; M59781; AAA22311.1; -.
EMBL; 29112; CAB13506.1; -.
EMBL; M86738; AAA22450.1; -.
EMBL; M87005; AAA22451.1; -.
PIR; A40894; A40874.
  Conservative
   Local Similarity
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August 13, 2003, 19:09:22 ; Search time 37 Seconds (without alignments) 948.518 Million cell updates/sec
  US-09-646-679-15
678
1 MATKSMGDIEKIKKKINVLI......LAKPLTKDKIIPLINQLMDA 136
  830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
   Total number of hits satisfying chosen parameters:
   830525 seqs, 258052604 residues
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
   sp_virus:*
sp_vertebrate:*
sp_unclassified:*
  sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
  sp_mhc:*
sp_organelle:*
  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
  sp_rodent:*
   sp_mammal:*
   Title:
Perfect score:
Sequence:
   Scoring table:
   Database :
  Searched:
   Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       |                     |                               |    | SUMMARIES |                    |
|---------------|-------|---------------------|-------------------------------|----|-----------|--------------------|
| Result<br>No. | Score | %<br>Query<br>Match | %<br>Query<br>Match Length DB | DB | QI.       | Description        |
|               | 678   | 100.0               | 136                           | 10 | 082445    | 082445 brassica na |
| 7             | 538   | 79.4                | 142                           | 10 | O9M8Y4    | Q9m8y4 arabidopsis |
| m             | 181   | 26.7                | 1969                          | S  | 015763    | 015763 dictyosteli |
| 4             | 179.5 | 26,5                | 820                           | 16 | Q8E263    | Q8ez63 leptospira  |
| Ŋ             | 178.5 | 26.3                | 1197                          | 16 | Q8CVU5    | Q8cvu5 escherichia |
| ω             | 174   | 25.7                | 394                           | 16 | Q9A3P0    | Q9a3p0 caulobacter |
| 7             | 173.5 | 25.6                | 949                           | 16 | OSFFP9    | Q8ffp9 escherichia |
| œ             | 173   | 25.5                | 417                           | ~  | Q9RLC7    | Q9rlc7 pseudomonas |
| ወ             | 171.5 | 25.3                | 933                           | 16 | Q8XE39    | Q8xe39 escherichia |
| 10            | 171.5 | 25.3                | 957                           | 16 | Q8ZGR4    | Q8zgr4 yersinia pe |
| 11            | 171   | 25.2                | 927                           | 7  | 09ANY0    | Q9any0 vibrio fisc |
| 12            | 170   | 25.1                | 769                           | 16 | Q8PQ37    | Q8pq37 xanthomonas |
| 13            | 167.5 | 24.7                | 1364                          | 16 | Q8PJN8    | Q8pjn8 xanthomonas |
| 14            | 166.5 | 24.6                | 507                           | N  | 085663    | 085663 proteus mir |
| 15            | 163.5 | 24.1                | 1364                          | 16 | Q8P883    | Q8p883 xanthomonas |
| 16            | 162.5 | 24.0                | 642                           | 16 | 09A3L2    | 09a312 caulobacter |

| Q9p896 emericella | Q8zb69 yersinia pe | Q8pd62 xanthomonas | Q9gtuO dictyosteli | 095ph5 dictyosteli | Q8d5i6 vibrio vuln | Q8d9h9 vibrio vuln | Q8dael vibrio vuln | 028381 archaeoglob | Q9kr16 vibrio chol | Q8yyw3 anabaena sp | Q8n1v2 neurospora |     |     |     |     | Q8qkv7 ectocarpus |       | Q9ks16 vibrio chol | Q9c1q7 aspergillus | m   | Q9a472 caulobacter | Q8kws5 marinomonas | Q8kgv0 vibrio chol | Q48299 halobacteri | Q9abt2 caulobacter | Q8ebg2 shewanella | ď        | Q8pmz3 xanthomonas |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-----|-----|-----|-----|-------------------|-------|--------------------|--------------------|-----|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|----------|--------------------|
| ٣                 | 16                 | ٦                  | ហ                  | Ŋ                  | 16                 | 16                 | 16                 | 17                 | 16                 | 16                 | ٣                 | 16  | ~1  | 17  | 16  | 12                | 17    | _                  | m                  | 7   | 16                 | ~                  | ~                  | 17                 | 16                 | 16                | 7        | 16                 |
| 0                 | ٥.                 | 3.9                | 3.8                | ω.                 | 3.7                | 3.7                | 3.5                | 'n                 | 3.5                | 3.5                | 3.4               | 3.2 | 3.1 | 3.0 | 2.9 | 6.                | 2.8   | 8.                 | 2.7                | 2.7 | 9.                 | 2.6                | ω.                 | 'n                 | ιυ.                | 2.5               | 22.5 935 | ٠.<br>د            |
| 162.5             | 162.5              | 162                | s.                 | s.                 | 51                 | 'n                 | 'n.                | 159                | 59                 |                    | r.                | 57  | 5.  | 99  | 155 | 155               | 154.5 | 154.5              | 154                | 54  | ر.<br>در           | ٦.                 | ۳                  |                    | ın                 | ın                | 2        | 152.5              |
| 17                | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28                | 29  | 30  | 31  | 32  | 33                | 34    |                    | 36                 | 37  | 38                 | 39                 | 40                 | 41                 | 42                 | 43                | 44       | 45                 |

# ALIGNMENTS

|                          |                                                              |                                                  |                                                                    |                                                                                                                            |                  |                           |                                                    |                                                           |                                                                                                   |        |                                    |                              |                                   |                                                                   |                                        |                                   |                   | 0;                                                      | 09 5                                                       | 9 60                                                        | P 120                                                        | P 120                                                        |
|--------------------------|--------------------------------------------------------------|--------------------------------------------------|--------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------|------------------|---------------------------|----------------------------------------------------|-----------------------------------------------------------|---------------------------------------------------------------------------------------------------|--------|------------------------------------|------------------------------|-----------------------------------|-------------------------------------------------------------------|----------------------------------------|-----------------------------------|-------------------|---------------------------------------------------------|------------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|
|                          |                                                              |                                                  | yta;                                                               | osidae                                                                                                                     |                  |                           |                                                    | ST STA                                                    |                                                                                                   |        |                                    |                              |                                   |                                                                   |                                        |                                   |                   | Gaps                                                    | IHRDGG                                                     | IHRDGG                                                      | NHCLAK                                                       | NHCLAK                                                       |
|                          |                                                              |                                                  | heoph                                                              | ts; R                                                                                                                      |                  |                           | Roberta J.A.;                                      | a s                                                       |                                                                                                   |        |                                    |                              |                                   |                                                                   |                                        |                                   | 136;              | 0;                                                      | SEEAVI                                                     | SEEAVI                                                      | PMEAGL                                                       | MEAGL                                                        |
|                          |                                                              |                                                  | ı, Trac                                                            | endico                                                                                                                     |                  |                           | Robert                                             | ממשומ                                                     | ases.                                                                                             |        |                                    |                              |                                   |                                                                   |                                        | 164;                              | Length 136;       | Indels                                                  | SQTANNO                                                    | SQTANN                                                      | SEERRAI                                                      | BERRA!                                                       |
|                          | Created)<br>Last sequence update)<br>Last annotation update) |                                                  | ophyte                                                             | core                                                                                                                       |                  |                           | V.M.                                               | ILCIII                                                    | r datak                                                                                           |        |                                    |                              |                                   |                                                                   |                                        | 15055 MW; DA99B768FAB3CFF5 CRC64; |                   |                                                         | KAIGGIS                                                    | KAIGGI                                                      | rsladni                                                      | SLADN                                                        |
| 136 AA.                  | .ed)<br>sequence update)<br>annotation updat                 |                                                  | Embry                                                              | edons;<br>Brass                                                                                                            |                  |                           | aylor                                              | roreir                                                    | k /DDB.                                                                                           |        |                                    |                              |                                   | -                                                                 |                                        | FAB3C                             | Score 678; DB 10; | 4.7e                                                    | HEKII                                                      | HEKII                                                       | SMIVGV                                                       | SMIVGV                                                       |
|                          | ed)<br>seguen<br>annota                                      |                                                  | phyta;                                                             | icotyl<br>aceae;                                                                                                           |                  |                           | .S.                                                | ator r                                                    | nt.";<br>GenBar                                                                                   |        |                                    |                              |                                   | TORY                                                              | tion.                                  | 99B768                            | re 678            | Pred. No. 4.<br>0; Mismatches                           | PLNLI                                                      | PLNLI                                                       | EMEVE                                                        | EMEVK                                                        |
| PRT;                     |                                                              |                                                  | trepto                                                             | a; eud<br>rassic                                                                                                           |                  |                           | kins B                                             | regut                                                     | eropme<br>EMBL/                                                                                   |        | se_reg                             | ; I:                         | reg; l                            | PEGIILA                                                           | ansduc                                 | W; DA                             |                   |                                                         | LIVDDE                                                     | TIVDDC                                                      | TTKKLF                                                       | TTKKLF                                                       |
| έ¥;                      | L. 08,                                                       | protein.                                         | cae; S                                                             | lophyte<br>les; B                                                                                                          |                  |                           | ., Jen                                             | sponse                                                    | to the                                                                                            | 225.1; | Respon                             | se_reg                       | _esuod                            | DONGE                                                             | orv tr                                 | 5055 M                            | 100.08;           | 100.0%<br>ive                                           | KKKLNV                                                     | KKKLNV                                                      | ERDGVS                                                       | ERDGVS                                                       |
| PRELIMINARY;             | (TremBLrel. 08, (TremBLrel. 08, (TremBLrel. 22,              | Response regulator pro-<br>Brassica papie (Rape) | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;<br>eurosids II; Brassicales; Brassicaceae; Brassica. |                  | Ą.                        | Whitelaw C.A., Paul W., Jenkins E.S., Taylor V.M., | encoding a response regulator protein irom brassica mapus | up-regulated during pod development.";<br>Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases | AAC 62 | InterPro; IPR001789; Response_reg. | Pfam; PF00072; response_reg; | Probom; PD000039; Response_reg; 1 | SMAKI; SMUU448; KEC; I.<br>DROSIDR. DASO110. RESPONSE RESILATORY: | Phosphorylation: Sensory transduction. | AA; 1                             |                   | Best Local Similarity 100.<br>Matches 136; Conservative | MATKSMGDIEKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIHRDGGS | MATKSMGDIEKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGS | SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNERERRAFMEAGLNHCLAKP | SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP |
| PREI                     |                                                              | თ ⊆                                              | Viri                                                               | iyta; l                                                                                                                    | =3708            | ROM N                     | A                                                  | COGIN                                                     | (APR-                                                                                             | 7027;  | IPROO                              | 072;                         | 000003                            | 0448;                                                             | 10.1                                   | 136 AA;                           | :                 | milar<br>Con                                            | AATKSM                                                     | ATKSM                                                       | SFDLIL                                                       | SFDLIL                                                       |
| 10 i                     | 01-NOV-1998<br>01-NOV-1998<br>01-NOV-1998<br>01-OCT-2002     | Response regulator<br>Brassica papus (Ran        | ryota;                                                             | matoph<br>sids I                                                                                                           | NCBI_TaxID=3708; | LIJ<br>SEGUENCE FROM N.A. | elaw C                                             | "A MRNA en                                                | egulat<br>itted                                                                                   | ; AF05 | rPro;                              | ; PF00                       | om; PC                            | SMART; SMUU448;                                                   | phore.                                 | SEQUENCE                          | atch              | cal Si<br>136;                                          | -                                                          | 7                                                           | 61 8                                                         | 61                                                           |
| JLT 1<br>445<br>082445   | ŽŽÖ-100                                                      | Resp                                             | Euka                                                               | Sper                                                                                                                       | NCBI             | SEOU                      | Whit                                               | E A                                                       | up-r                                                                                              | EMBL   | Inte                               | Pfam                         | ProD                              | SMAR                                                              | pho a                                  | SEQU                              | Query Match       | est Lc<br>atches                                        |                                                            |                                                             |                                                              |                                                              |
| RESULT<br>082445<br>ID 0 | 2555                                                         | DE                                               | 88                                                                 | 88                                                                                                                         | ŏ                | X X<br>V                  | RA                                                 | K I                                                       | E E                                                                                               | N.     | DR                                 | DR                           | H H                               | ¥ 6                                                               | 3 3                                    | SO                                | Ø                 | ω Σ                                                     | Qy                                                         | QC                                                          | οy                                                           | q                                                            |

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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hybrid histidine kinase DHKB.
  ||: | | :| :|
1951 QKPIKTSDILIQMI 1964
  Q8EZ63;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
  118 AKPL-TKDKIIPLI 130
  Best Local Similarity 35.89
Matches 48; Conservative
  PRELIMINARY;
   SEQUENCE FROM N.A.
  Query Match
  Q8EZ63
   RESULT 4
Q8EZ63
 염
  δ
   d
  ò
  g
   55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
   54
  1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII
   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
   Gaps
   STRAIN-CV. Columbia;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC TGRIZ genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
   9
  SEQUENCE FROM N.A.

Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome annotation.";
Genome Biol. 0:0-0(2002).
  SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
  Length 142;
  79.4%; Score 538; DB 10; Length 1 78.9%; Pred. No. 9.8e-40; rative 8; Mismatches 16; Indels
   Putative response regulator protein (receiver component).
   "Full Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC16829; AAR26786.1; -.
EMBL; AY085638; AAM62859.1; -.
InterPro; IPR001789; Response_reg.
  Pfan; PF00072; response_reg; 1.
Prodom; PD000039; Response_reg; 1.
PROSITE; P550110; RESPONSE_REGULATORY; 1.
Phosphorylation; Sensory transduction.
SEQUENCE 142 AA; 15792 MW; 57487135FF2D5238 CRC64;
  Last sequence update)
Last annotation update)
   Created)
Last sequence update)
   142 AA.
  PRT; 1969 AA.
  Created)
  121 HCLEKPLTKAKIFPLISHLFDA 142
  115 HCLAKPLTKDKIIPLINQLMDA 136
   PRT;
                                     121 LTKDKIIPLINQLMDA 136
                 121 LTKDKIIPLINQLMDA 136
  015763 PRELIMINARY;
015763;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
  01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
   Matches 112; Conservative
  Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
   Q9M8Y4;
   Q9M8Y4
  RESULT 3
015763
  RESULT 2
Q9M8Y4
```

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70 EMPERDGVSTTKKLREMEVKSMI-----VGVTSLADNE--EERRAFMEAGLNHCL 117
   10 EKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDK 69
   A zinda M.J., Singieton C.K.;

Inda M.J., Singieton C.K.;

Inde hybrid histidine kinase dhkB regulates spore germination in Divoystellum discoldeum.;

In Dev. Byori. 196:171-183 (198).

R mbl., APC24654; AAA71889.1; ---

R interPro; IPR004559; ATPbind_ATPase.

R interPro; IPR00559; His_kinA.

R interPro; IPR00567; His_kinA.

R interPro; IPR001789; Response_reg.

R interPro; IPR001789; Response_reg.

R interPro; IPR001789; Response_reg.

R interPro; IPR001789; Response_reg.

R Pfam; PF00512; HisKA; I.

R Probom; PR000034; Response_reg; I.

R Probom; PR000034; Response_reg; I.

R RAART; SM00389; HATPase_c; I.

R SMART; SM00389; HATPase_c; I.

R SMART; SM00091; PAS; I.
   Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
  Length 1969;
   SEQUENCE FROM N.A.
STRAIN-56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
   PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGILATORY; 1.
Kinase: Phosphorylation; Sensory transduction.
SEQUENCE 1969 AA; 219025 MW; BE7A7952AB1BB52B CRC64;
   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB011554; AAN51193.1; -.
Complete protecome.
SEQUENCE 820 AA; 94325 MW; 3DBE99966794E67D CRC64;
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Two-component hybrid sensor and regulator.
  26.7%; Score 181; DB 5; 35.8%; Pred. No. 5.1e-07;
  29; Mismatches
   TIGRFAMS; TIGR00229; sensory_box; 1.
   PRT;
   STRAIN=KAx3;
MEDLINE=98248997; Pubmed=9576830;
   AC OCC OCC SENT REPRESENTATION
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3

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7
  1013 PNMDGFELTRKLÆEGNSSLPIWGLTANA-QANEREKGLNCGMNLCLFKPLTLDVLKTHLS 1071
                                  'n
  72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
  DLILMDKEMPERDGVSTTKKLREMEVKS---MIVGVTSLADNEEERRAFMEAGLNHCLAK 119
  71
  62
  STRAIN-06:HI / CFT073 / ATCC 700928;
MEDLINE-22388234; PubMed-12471157;
WEDLINE-22388234; PubMed-12471157;
WEDLINE-22388234; PubMed-12471157;
WEDLINE-22388234; PubMed-12471157;
WEDLINE-22388234; PubMed-12471157;
WESKO D., Buckles E.L., Liduo S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
  12 IKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM
  8 DIEK----IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSF
                                  Gaps
  Gaps
  EVGS OR C2906.
Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
  26.3%; Score 178.5; DB 16; Length 1197; 34.4%; Pred. No. 4.6e-07; Live 25; Mismatches 52; Indels 3;
                                  15;
 DB 16; Length 820;
                                  49; Indels
   Transferase, Complete proteome.
SEQUENCE 1197 AA, 134847 MW, 5088214E7F834F06 CRC64;
   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
CC3162.
CC3162.
Caulobacter crescentus.
  01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Sensor protein evgs precursor (EC 2.7.3.-).
ch 26.5%; Score 179.5; DB 1
I Similarity 31.6%; Pred. No. 2.4e-07;
43; Conservative 29; Mismatches 49
  394 AA.
  1197 AA
   01-MAR-2003 (TrEMBLrel. 23, Created)
  PRT;
  PRT;
   120 PLTKDKIIPLINQLMD 135
   PLD----LPILKSTLD 807
   Best Local Similarity 34.49
Matches 42; Conservative
  PRELIMINARY;
  PRELIMINARY;
 Query Match
Best Local Similarity
   SEQUENCE FROM N.A.
   1072 QL 1073
  132 QL 133
   63
   Query Match
  Q9A3P0;
  09A3P0
   RESULT 6
Q9A3P0
                                  Matches
  RESULT 5
Q8CVU5
  ID DAY OF DAY OS OS
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   qq
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  Д
  g
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74 RDGVSTTKKLREMEVKSMIVGVTSLADNEE -- ERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
   SEQUENCE FROM N.A.

C STRIN-ATCC 19089 / CB15;

A MEDLINE-21173698; Pubmed=11259647;

A Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

A Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N.D., Ely B.,

A Deboy R.T., Dodson R.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

T. Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(201).

REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

RASSP, PO6657; 204F.

RESSP, PO6657; 204F.
  14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
   STRAIN=06:HI / CFT073 / ATCC 700928;
MEDLINE=2238024; PubMed=1247157;
WHOTCH R., BULIAGO V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Extensive mosaic structure revealed by the complete genome sequence
   4; Gaps
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  transduction; Complete proteome.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
  Length 394;
   Query Match
25.7%; Score 174; DB 16; Length 39
Best Local Similarity 31.7%; Pred. No. 3.1e-07;
Matches 39; Conservative 31; Mismatches 49; Indels
   Kinase, Phosphorylation; Sensory transduction; Complet.
SEQUENCE 394 AA; 41592 MW; 6D9AF0B278B70E70 CRC64;
  Last sequence update)
Last annotation update)
   PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
  InterPro: IPR003594; ATPbind_ATPase.
InterPro: IPR003594; His_Kinase.
InterPro: IPR001789; Response_reg.
Ffan; PF02518; HATPase_c; 1.
Ffam; PF00072; response_reg; 1.
SMART; SM0039; Response_reg; 1.
SMART; SM00387; HATPase_c; 1.
  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
Sensor protein rcsC (EC 2.7.3.)
  Enterobacteriaceae; Escherichia
  PRELIMINARY;
   Escherichia coli 06
  NCBI_TaxID=217992;
  SEQUENCE FROM N.A.
   132 QLM 134
  380 SLL 382
   RCSC OR C2761
   Q8FFP9;
  Q8FFP9
   RESULT 7
08FFP9
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Yersinia pestis
  SEQUENCE
  Query Match
   Q8ZGR4
   RESULT 10
Q8ZGR4
   SOUR DE REAL D
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  92
  18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFDLILMDKEMPERDG 76
  77 VSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLI 130
  17 NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG
  Gaps
  77 VSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
  Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amotation update)
Sensor for ctr capsule biosynthesis, probable histidine kinase acting on RcsB.

RCSC OR 2477 OR ECS3107.

Escherichia coli 0157:H7.
   884 YRLTQRIRQLGLTLPVIGVTANALAEEKQRC-LESGMDSCLSKPVTLDVI 932
  'n
  25.6%; Score 173.5; DB 16; Length 949; 33.6%; Pred. No. 9.7e-07; Live 35; Mismatches 33; Indels 5;
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   Graupner S., Wackernagel W.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249/41; CAB56474.1;
InterPro; IPR0012570; Hpt. .
InterPro; IPR0011789; Response_reg.
Pfam: PF00072; response_reg; 1.
ProDom: PD000039; Response_reg; 1.
                                  Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL: AE016763; AAN81215.1; -
Transferase; Complete proteome.
SEQUENCE 949 AA; 106590 WW; DF8CA47F9EEB4088 CRC64;
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Kinase; Phosphorylation; Sensory transduction.
NON_TER 1 1 1 1 SEQUENCE 417 AA; 45749 MW; D196B4FFDDA23BB2 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
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   933 AA
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uropathogenic Escherichia coli.";
  Best_Local Similarity 33.69
Matches 37; Conservative
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SMART; SM00448; REC; 1
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  STRAIN-JM300;
  Query Match
   Query Match
   Q8XE39
  . 08XE39
   Q9RLC7
   Matches
   RESULT 8
   RESULT ORKES OF STATE
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811 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 868
  18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETALINE-15:17 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tobe T., Takami H. Enda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genomes sequence of enterohemorrhagic Escherichia coli 015:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL: AP005560; BAB365333:1;
HSSP: P06143; 1D42.
   Gaps
   "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotcheck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
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e
  STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
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01-MAR-2002 (TrEMBLrel. 20, Created)

01-MAR-2003 (TrEMBLrel. 20, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

01-MAR-2003 (TrEMBLrel. 20, Last annotat
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es 37;
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33.9%; Pred. No. 1.4e
iive 32; Mismatches
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PROSITE; PS50110; RESPONSE_REGULATORY; 1.
  Interpro; IPR003594, ATPbind_ATPase.
Interpro; IPR004358; Bact_sens_pr_C.
Interpro; IPR00561; His_KinA.
Interpro; IPR005057; His_Kinase.
Interpro; IPR001014; PAS_domain.
Interpro; IPR001789; Response_reg.
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   PRINTS; PR00344; BCTRLSENSOR.
Prodom; PD000039; Response_reg; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; Hiska; 1.
SMART; SM0091; PAS; 1.
  ; response_reg; 1.
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Pfam; PF00512; HisKA; 1.
   Kinase, Complete proteome
   Local Similarity 33.9
nes 37; Conservative
   PRELIMINARY;
   SMART; SM00448; REC;
   SEQUENCE FROM N.A.
  Pfam; PF00072
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MEDLINE=21142508; PubMed=11208780;
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   08P037
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Q8PQ37
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  SECURENCE FROM NA.

STRAIN=KINS / Blovar Mediaevalis;

XR STRAIN=KINS / Blovar Mediaevalis;

XR EDLINE-22137863; PubMed-12142430;

XR EDLINE-22137863; PubMed-12142430;

XR EDLINE-22137863; PubMed-12142430;

XR ETHERSTON V. PIUNKEtt G. III, Boutin A., Mayhew G.F., Liss P.,

AB PETRA N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

AR STARIEY S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

AR PETRA R.D.;

AR Genome sequence of Yersinia pestis KIM.";

AR Genome sequence of Yersinia pestis KIM.";

AR BENEL, AJ41417; CAC90055.1;

BENEL, AJ41417; CAC90055.1;

BENEL, ALOHISB98; AAM86522.1;

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RICHEPPO: IPRO03594; ATPDING_ATPASE.

RICHEPPO: IRRO03561; His_Kinase.

RICHEPPO: IRRO03561; His_Kinase.

RICHEPPO: IRRO036189; Response_reg.
   892
   16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
   MEDLINE=21470413; PubMed=11586360; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Drentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chilingworth T., Cronin A., Davies R.W., Davis P., Dougan G., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Mature 413:523-527(2001).
  Gaps
  76 GVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
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Vibrio fischeri.
Vibrionaceae; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=668;
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Prodom; PD000039; Response_reg; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS501109; RESPONSE REGULATORY; 1.
Kinase, Transferase; Complete proteome.
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Pfam; PF00072; response_reg; 1.
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  Query Match
Best Local Similarity 35.1%
Matches 39; Conservative
  PRELIMINARY;
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SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
                               NCBI_TaxID=632;
  OBANYO;
  Q9ANY0
   RSCS.
  RESULT 11
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76 GVSTIKKLRE-MEVKSMIVGVTSLA----DNEEERRAFWEAGLNHCLAKPLIKDKIIPL 129
   75
   16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD
   14; Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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  Length 927;
  42; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Two-component system sensor protein.
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33.9%; Pred. No. 1.6e-06;
iive 28; Mismatches 42;
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STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
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   130 INQLMDA 136
  771 IKQYQDA 777
   NCBI_TaxID=92829;
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Query Match
   085663
   RESULT 14
085663
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            da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Ouaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
A. Alves L.M.C., do Amaral A.M., Bertolii M.C., Camargo L.E.A.,
R.A. Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
R.A. Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
A. Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
R.A. Formidhieri E.F., Franco M.C., Greggio C.C., Ferro M.I.T.,
R. Formidhieri E.F., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,
Martins E.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
R. Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
R. Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,
R. Spinola L.A.F., Takita M.A., Tanmura R.E., Teixeira E.C., Tezza R.I.D.,
R. Stubal J.C., Kitajima J.P.;
R. "Comparison of the genomes of two Xanthomonas pathogens with differing
Nature Repetificities ""
   14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
  74 RDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFWEAGLNHCLAKPLTKDKI 126
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da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
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Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos Jr.K., El-Dorry H.A.,
Faria J.B., Ferreira R.C.C., Ferro M.I.T.,
Ferriga J.B., Ferreira R.C.C., Greggio C.C., Gruber A.,
   Xanthomonas axonopodis (pv. citri).
Bacteria; Vanthomonadales;
Xanthomonadaceae; Xanthomonas.
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8
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Last sequence update)
Last annotation update)
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ProDom; PD000039; Response_reg; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
   Nature 417:459-463(2002).
Nature 417:459-463(2002).
INTERPO. 1PR003594: AAPDAIG_ATBASE.
INTERPO. IPR004358; Bact_sens_pr_C.
INTERPO. IPR0003661; His_KinA.
INTERPO. IPR005467; His_KinA.
INTERPO. IPR005467; His_KinA.
INTERPO. IPR001789; Response_reg.
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   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 30.5%
Matches 36; Conservative
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   Complete proteome. SEQUENCE 769 AA;
  Q8PJN8;
  RESULT 13
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Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,

Amartins E.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,

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Pereira H.A., Rossi A., Sena J.D., Silva C., de Souza R.F.,

R.A. Spinola L.A.F., Takita M.A., Tamura R.E., Takiza B.C., Tezza R.I.D.,

R.A. Trindade dos Santos M. Truffi D., Tsai S.M., White F.F.,

R. Trindade dos Santos M. Truffi D., Tsai S.M., White F.F.,

R. Trindade dos Santos M. Truffi D., Tsai S.M., White F.F.,

R. Mature 417:459-463(2002)

R. InterPro: IPR004198; Bact_sens_Pr_C.

InterPro: IPR004198; Bact_sens_Pr_C.

InterPro: IPR004198; Bact_sens_Pr_C.

R. InterPro: IPR001099; Pac.

InterPro: IPR001099; Pac.

InterPro: IPR001099; Response_reg.

InterPro: IPR001199; Response_reg.

R. Ffam: PF00181; Haxki I.

R. Ffam: PF001819; Response_reg; 2.

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R. Ffam: PF00189; Response_reg; 2.

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  1093 YEATRRIRQIPALASLEVIALTAGAFRPQQEKA-LEAGMNGFIAKPFNVEELVTAIRHFL 1151
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   STRAIN-BB2000), MEDLINE-99047557; PubMed-9829920; Belas R., Schneider R., Melch M.; Belas R., Schneider R., Choreus mirabilis precocious swarming mutants: "Characterization of Proteus mirabilis precocious swarming behavior."; identification of rsbA, encoding a regulator of swarming behavior.";
   Proteus mirabilis
Bacteria; proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Last annotation update)
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Matches 35; Conservative
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   RcsC (Fragment)
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SEQUENCE FROM N.A.

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RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almielda N.F.,

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RA Alves L.M.C., Countho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

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RA Locali B.C., Mediado M.A., Madeira A.M.B.N., Martines Rossi N.M.,

RA Martins E.C., Medianis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

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RA Setubal J.C., Ritajima J.P.,

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RA Dereira R.C., Mitajima 
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Bacteria, Forteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBL_TaxID=340;
   ŝ
  | :||: |:||: |:||: | 455 GYQLATTVRELSSTIPIIGVTANAIABERQRC-IDAGMNDCVSKPVS 500
  76 GVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLT 122
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PRINTS, PRO034, 1976-197.

Prodom, PRO039; Response_reg; 1.

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SMART; SM00448; REC; 1.

PROSITE; PS50109; HIS_KIN; 1.

PROSITE; PS50109; RESPONSE_REGULATORY; 1.

Kinase; Phosphorylation; Sensory transduction; Transferase.
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Last annotation update)
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Pfam; PP00012; response_reg; 1.
  Created)
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    180:6126-6139(1998)
  EMBL; AF071215; AAC82662.1; -. HSSP; P06657; 2CHF.
  01-OCT-2002 (TrEMBLrel, 22, 01-OCT-2002 (TrEMBLrel, 22, 01-MAR-2003 (TrEMBLrel, 23,
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Matches 39; Conservative
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  NON_TER
SEQUENCE
   RESULT 15
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      q
   δ
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18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
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|-----|---------|-----------------|
|     | SRNT    | 94              |

Total number of pages: 94

Remarks:

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